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(54) Title: **MOLECULES FOR DISEASE DETECTION AND TREATMENT**

(57) Abstract: The present invention provides purified disease detection and treatment molecule polynucleotides (mddt). Also encompassed are the polypeptides (MDDT) encoded by mddt. The invention also provides for the use of mddt, or complements, oligonucleotides, or fragments thereof in diagnostic assays. The invention further provides for vectors and host cells containing mddt for the expression of MDDT. The invention additionally provides for the use of isolated and purified MDDT to induce antibodies and to screen libraries of compounds and the use of anti-MDDT antibodies in diagnostic assays. Also provided are microarrays containing mddt and methods of use.



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## TECHNICAL FIELD

The present invention relates to molecules for disease detection and treatment and to the use of these sequences in the diagnosis, study, prevention, and treatment of diseases associated with, as well as effects of exogenous compounds on, the expression of molecules for disease detection and treatment.

## BACKGROUND OF THE INVENTION

The human genome is comprised of thousands of genes, many encoding gene products that function in the maintenance and growth of the various cells and tissues in the body. Aberrant expression or mutations in these genes and their products is the cause of, or is associated with, a variety of human diseases such as cancer and other cell proliferative disorders. The identification of these genes and their products is the basis of an ever-expanding effort to find markers for early detection of diseases, and targets for their prevention and treatment.

For example, cancer represents a type of cell proliferative disorder that affects nearly every tissue in the body. A wide variety of molecules, either aberrantly expressed or mutated, can be the cause of, or involved with, various cancers because tissue growth involves complex and ordered patterns of cell proliferation, cell differentiation, and apoptosis. Cell proliferation must be regulated to maintain both the number of cells and their spatial organization. This regulation depends upon the appropriate expression of proteins which control cell cycle progression in response to extracellular signals such as growth factors and other mitogens, and intracellular cues such as DNA damage or nutrient starvation. Molecules which directly or indirectly modulate cell cycle progression fall into several categories, including growth factors and their receptors, second messenger and signal transduction proteins, oncogene products, tumor-suppressor proteins, and mitosis-promoting factors. Aberrant expression or mutations in any of these gene products can result in cell proliferative disorders such as cancer. Oncogenes are genes generally derived from normal genes that, through abnormal expression or mutation, can effect the transformation of a normal cell to a malignant one (oncogenesis). Oncoproteins, encoded by oncogenes, can affect cell proliferation in a variety of ways and include growth factors, growth factor receptors, intracellular signal transducers, nuclear transcription factors, and cell-cycle control proteins. In contrast, tumor-suppressor genes are involved in inhibiting cell proliferation. Mutations which cause reduced or loss of function in tumor-suppressor genes result in aberrant cell proliferation and cancer. Thus a wide variety of genes and their products have been found that are associated with cell proliferative disorders such as cancer, but many more may exist that are yet to be discovered.

DNA-based arrays can provide a simple way to explore the expression of a single

polymorphic gene or a large number of genes. When the expression of a single gene is explored, DNA-based arrays are employed to detect the expression of specific gene variants. For example, a p53 tumor suppressor gene array is used to determine whether individuals are carrying mutations that predispose them to cancer. A cytochrome p450 gene array is useful to determine whether individuals have one of a number of specific mutations that could result in increased drug metabolism, drug resistance or drug toxicity.

DNA-based array technology is especially relevant for the rapid screening of expression of a large number of genes. There is a growing awareness that gene expression is affected in a global fashion. A genetic predisposition, disease or therapeutic treatment may affect, directly or indirectly, the expression of a large number of genes. In some cases the interactions may be expected, such as when the genes are part of the same signaling pathway. In other cases, such as when the genes participate in separate signaling pathways, the interactions may be totally unexpected. Therefore, DNA-based arrays can be used to investigate how genetic predisposition, disease, or therapeutic treatment affects the expression of a large number of genes.

The discovery of new molecules for disease detection and treatment satisfies a need in the art by providing new compositions which are useful in the diagnosis, study, prevention, and treatment of diseases associated with, as well as effects of exogenous compounds on, the expression of molecules for disease detection and treatment.

## **SUMMARY OF THE INVENTION**

The present invention relates to human disease detection and treatment molecule polynucleotides (mddt) as presented in the Sequence Listing. The mddt uniquely identify genes encoding structural, functional, and regulatory disease detection and treatment molecules.

The invention provides an isolated polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-396; b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-396; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). In one alternative, the polynucleotide comprises a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-396. In another alternative, the polynucleotide comprises at least 30 contiguous nucleotides of a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-396; b) a polynucleotide comprising a naturally occurring polynucleotide comprising a polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-396; c) a polynucleotide



complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). In another alternative, the polynucleotide comprises at least 60 contiguous nucleotides of a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-396; b) a polynucleotide comprising a naturally occurring polynucleotide comprising a polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-396; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). The invention further provides a composition for the detection of expression of disease detection and treatment molecule polynucleotides comprising at least one isolated polynucleotide comprising a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-396; b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-396; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d); and a detectable label.

The invention also provides a method for detecting a target polynucleotide in a sample, said target polynucleotide having a polynucleotide sequence of a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence of a polynucleotide selected from the group consisting of SEQ ID NO:1-396; b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-396; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). The method comprises a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

The invention also provides a method for detecting a target polynucleotide in a sample, said target polynucleotide having a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-396; b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-396; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). The method comprises a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target

polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide, and b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof. In one alternative, the invention provides a composition comprising a target polynucleotide of the method, wherein said probe comprises at least 30 contiguous nucleotides. In one alternative, the invention provides a composition comprising a target polynucleotide of the method, wherein said probe comprises at least 60 contiguous nucleotides.

The invention further provides a recombinant polynucleotide comprising a promoter sequence operably linked to an isolated polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-396; b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-396; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). In one alternative, the invention provides a cell transformed with the recombinant polynucleotide. In another alternative, the invention provides a transgenic organism comprising the recombinant polynucleotide.

The invention also provides a method for producing a disease detection and treatment molecule polypeptide, the method comprising a) culturing a cell under conditions suitable for expression of the disease detection and treatment molecule polypeptide, wherein said cell is transformed with a recombinant polynucleotide, said recombinant polynucleotide comprising an isolated polynucleotide selected from the group consisting of i) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-396; ii) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-396; iii) a polynucleotide complementary to the polynucleotide of i); iv) a polynucleotide complementary to the polynucleotide of ii); and v) an RNA equivalent of i) through iv), and b) recovering the disease detection and treatment molecule polypeptide so expressed. The invention additionally provides a method wherein the polypeptide has an amino acid sequence selected from the group consisting of SEQ ID NO:397-792pp range - upper pp range].

The invention also provides an isolated disease detection and treatment molecule polypeptide (MDDT) encoded by at least one polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-396. The invention further provides a method of screening for a test compound that specifically binds to the polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:397-792. The method comprises a) combining the polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:397-792 with at least one test compound under suitable conditions, and b) detecting binding of the polypeptide having

an amino acid sequence selected from the group consisting of SEQ ID NO:397-792 to the test compound, thereby identifying a compound that specifically binds to the polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:397-792.

The invention further provides a microarray wherein at least one element of the microarray is  
5 an isolated polynucleotide comprising at least 30 contiguous nucleotides of a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-396; b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-396; c) a polynucleotide complementary to the polynucleotide of a); d) a  
10 polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). The invention also provides a method for generating a transcript image of a sample which contains polynucleotides. The method comprises a) labeling the polynucleotides of the sample, b) contacting the elements of the microarray with the labeled polynucleotides of the sample under conditions suitable for the formation of a hybridization complex, and c) quantifying the expression of the polynucleotides  
15 in the sample.

Additionally, the invention provides a method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-396; b) a polynucleotide comprising a  
20 naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-396; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). The method comprises a) exposing a sample comprising the target polynucleotide to a compound, b) detecting altered expression of the target polynucleotide, and c)  
25 comparing the expression of the target polynucleotide in the presence of varying amounts of the compound and in the absence of the compound.

The invention further provides a method for assessing toxicity of a test compound, said method comprising a) treating a biological sample containing nucleic acids with the test compound; b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20  
30 contiguous nucleotides of a polynucleotide selected from the group consisting of i) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-396; ii) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-396; iii) a polynucleotide complementary to the polynucleotide of i); iv) a polynucleotide complementary to the polynucleotide  
35 of ii); and v) an RNA equivalent of i) through iv). Hybridization occurs under conditions whereby a

specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide selected from the group consisting of i) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-396; ii) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-396; iii) a polynucleotide complementary to the polynucleotide of i); iv) a polynucleotide complementary to the polynucleotide of ii); and v) an RNA equivalent of i) through iv), and alternatively, the target polynucleotide comprises a polynucleotide sequence of a fragment of a polynucleotide selected from the group consisting of i-v above; c) quantifying the amount of hybridization complex; and d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

The invention further provides an isolated polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:397-792, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:397-792, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:397-792, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:397-792. In one alternative, the invention provides an isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:397-792.

The invention further provides an isolated polynucleotide encoding a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:397-792, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:397-792, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:397-792, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:397-792. In one alternative, the polynucleotide encodes a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:397-792. In another alternative, the polynucleotide comprises a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-396.

Additionally, the invention provides an isolated antibody which specifically binds to a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:397-792, b) a polypeptide comprising a naturally

occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:397-792, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:397-792, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:397-792.

The invention further provides a composition comprising a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:397-792, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:397-792, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:397-792, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:397-792, and a pharmaceutically acceptable excipient. In one embodiment, the composition comprises a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:397-792. The invention additionally provides a method of treating a disease or condition associated with decreased expression of functional MDDT, comprising administering to a patient in need of such treatment the composition.

The invention also provides a method for screening a compound for effectiveness as an agonist of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:397-792, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:397-792, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:397-792, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:397-792. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting agonist activity in the sample. In one alternative, the invention provides a composition comprising an agonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with decreased expression of functional MDDT, comprising administering to a patient in need of such treatment the composition.

Additionally, the invention provides a method for screening a compound for effectiveness as an antagonist of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:397-792, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:397-792, c) a biologically active fragment

of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:397-792, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:397-792. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting antagonist activity in the sample.

5 In one alternative, the invention provides a composition comprising an antagonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with overexpression of functional MDDT, comprising administering to a patient in need of such treatment the composition.

The invention further provides a method of screening for a compound that modulates the  
10 activity of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:397-792, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:397-792, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:397-792, and d) an  
15 immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:397-792. The method comprises a) combining the polypeptide with at least one test compound under conditions permissive for the activity of the polypeptide, b) assessing the activity of the polypeptide in the presence of the test compound, and c) comparing the activity of the polypeptide in the presence of the test compound with the activity of the polypeptide in the absence of  
20 the test compound, wherein a change in the activity of the polypeptide in the presence of the test compound is indicative of a compound that modulates the activity of the polypeptide.

## DESCRIPTION OF THE TABLES

Table 1 shows the sequence identification numbers (SEQ ID NO:s) and template identification  
25 numbers (template IDs) corresponding to the polynucleotides of the present invention, along with the sequence identification numbers (SEQ ID NO:s) and open reading frame identification numbers (ORF IDs) corresponding to polypeptides encoded by the template ID.

Table 2 shows the sequence identification numbers (SEQ ID NO:s) and template identification numbers (template IDs) corresponding to the polynucleotides of the present invention, along with their  
30 GenBank hits (GI Numbers), probability scores, and functional annotations corresponding to the GenBank hits.

Table 3 shows the sequence identification numbers (SEQ ID NO:s) and template identification numbers (template IDs) corresponding to the polynucleotides of the present invention, along with polynucleotide segments of each template sequence as defined by the indicated "start" and "stop"  
35 nucleotide positions. The reading frames of the polynucleotide segments and the Pfam hits, Pfam

descriptions, and E-values corresponding to the polypeptide domains encoded by the polynucleotide segments are indicated.

Table 4 shows the sequence identification numbers (SEQ ID NO:s) and template identification numbers (template IDs) corresponding to the polynucleotides of the present invention, along with  
5 polynucleotide segments of each template sequence as defined by the indicated "start" and "stop" nucleotide positions. The reading frames of the polynucleotide segments are shown, and the polypeptides encoded by the polynucleotide segments constitute either signal peptide (SP) or transmembrane (TM) domains, as indicated. For TM domains, the membrane topology of the encoded polypeptide sequence is indicated as being transmembrane or on the cytosolic or non-cytosolic side of  
10 the cell membrane or organelle.

Table 5 shows the sequence identification numbers and template identification numbers (/template IDs) corresponding to the polynucleotides of the present invention, along with component sequence identification spans corresponding to each template. The component sequences, which were used to assemble the template sequences, are defined by the spans indicating the nucleotide  
15 positions along each template.

Table 6 shows the tissue distribution profiles for the templates of the invention.

Table 7 shows the sequence identification numbers (SEQ ID NO:s) corresponding to the polypeptides of the present invention, along with the reading frames used to obtain the polypeptide segments, the lengths of the polypeptide segments, the "start" and "stop" nucleotide positions of the  
20 polynucleotide sequences used to define the encoded polypeptide segments, the GenBank hits (GI Numbers), probability scores, and functional annotations corresponding to the GenBank hits.

Table 8 summarizes the bioinformatics tools which are useful for analysis of the polynucleotides of the present invention. The first column of Table 8 lists analytical tools, programs, and algorithms, the second column provides brief descriptions thereof, the third column presents  
25 appropriate references, all of which are incorporated by reference herein in their entirety, and the fourth column presents, where applicable, the scores, probability values, and other parameters used to evaluate the strength of a match between two sequences (the higher the score, the greater the homology between two sequences).

## 30 DETAILED DESCRIPTION OF THE INVENTION

Before the nucleic acid sequences and methods are presented, it is to be understood that this invention is not limited to the particular machines, methods, and materials described. Although particular embodiments are described, machines, methods, and materials similar or equivalent to these embodiments may be used to practice the invention. The preferred machines, methods, and materials

set forth are not intended to limit the scope of the invention which is limited only by the appended claims.

The singular forms "a", "an", and "the" include plural reference unless the context clearly dictates otherwise. All technical and scientific terms have the meanings commonly understood by one of ordinary skill in the art. All publications are incorporated by reference for the purpose of describing and disclosing the cell lines, vectors, and methodologies which are presented and which might be used in connection with the invention. Nothing in the specification is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

## **Definitions**

As used herein, the lower case "mddt" refers to a nucleic acid sequence, while the upper case "MDDT" refers to an amino acid sequence encoded by mddt. A "full-length" mddt refers to a nucleic acid sequence containing the entire coding region of a gene endogenously expressed in human tissue.

"Adjuvants" are materials such as Freund's adjuvant, mineral gels (aluminum hydroxide), and surface active substances (lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, and dinitrophenol) which may be administered to increase a host's immunological response.

"Allele" refers to an alternative form of a nucleic acid sequence. Alleles result from a "mutation," a change or an alternative reading of the genetic code. Any given gene may have none, one, or many allelic forms. Mutations which give rise to alleles include deletions, additions, or substitutions of nucleotides. Each of these changes may occur alone, or in combination with the others, one or more times in a given nucleic acid sequence. The present invention encompasses allelic mddt.

An "allelic variant" is an alternative form of the gene encoding MDDT. Allelic variants may result from at least one mutation in the nucleic acid sequence and may result in altered mRNAs or in polypeptides whose structure or function may or may not be altered. A gene may have none, one, or many allelic variants of its naturally occurring form. Common mutational changes which give rise to allelic variants are generally ascribed to natural deletions, additions, or substitutions of nucleotides. Each of these types of changes may occur alone, or in combination with the others, one or more times in a given sequence.

"Altered" nucleic acid sequences encoding MDDT include those sequences with deletions, insertions, or substitutions of different nucleotides, resulting in a polypeptide the same as MDDT or a polypeptide with at least one functional characteristic of MDDT. Included within this definition are polymorphisms which may or may not be readily detectable using a particular oligonucleotide probe of the polynucleotide encoding MDDT, and improper or unexpected hybridization to allelic variants, with



a locus other than the normal chromosomal locus for the polynucleotide sequence encoding MDDT. The encoded protein may also be “altered,” and may contain deletions, insertions, or substitutions of amino acid residues which produce a silent change and result in a functionally equivalent MDDT. Deliberate amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues, as long as the biological or immunological activity of MDDT is retained. For example, negatively charged amino acids may include aspartic acid and glutamic acid, and positively charged amino acids may include lysine and arginine. Amino acids with uncharged polar side chains having similar hydrophilicity values may include: asparagine and glutamine; and serine and threonine. Amino acids with uncharged side chains having similar hydrophilicity values may include: leucine, isoleucine, and valine; glycine and alanine; and phenylalanine and tyrosine.

“Amino acid sequence” refers to a peptide, a polypeptide, or a protein of either natural or synthetic origin. The amino acid sequence is not limited to the complete, endogenous amino acid sequence and may be a fragment, epitope, variant, or derivative of a protein expressed by a nucleic acid sequence.

“Amplification” refers to the production of additional copies of a sequence and is carried out using polymerase chain reaction (PCR) technologies well known in the art.

“Antibody” refers to intact molecules as well as to fragments thereof, such as Fab, F(ab')<sub>2</sub>, and Fv fragments, which are capable of binding the epitopic determinant. Antibodies that bind MDDT polypeptides can be prepared using intact polypeptides or using fragments containing small peptides of interest as the immunizing antigen. The polypeptide or peptide used to immunize an animal (e.g., a mouse, a rat, or a rabbit) can be derived from the translation of RNA, or synthesized chemically, and can be conjugated to a carrier protein if desired. Commonly used carriers that are chemically coupled to peptides include bovine serum albumin, thyroglobulin, and keyhole limpet hemocyanin (KLH). The coupled peptide is then used to immunize the animal.

The term “aptamer” refers to a nucleic acid or oligonucleotide molecule that binds to a specific molecular target. Aptamers are derived from an *in vitro* evolutionary process (e.g., SELEX (Systematic Evolution of Ligands by EXponential Enrichment), described in U.S. Patent No. 5,270,163), which selects for target-specific aptamer sequences from large combinatorial libraries. Aptamer compositions may be double-stranded or single-stranded, and may include deoxyribonucleotides, ribonucleotides, nucleotide derivatives, or other nucleotide-like molecules. The nucleotide components of an aptamer may have modified sugar groups (e.g., the 2'-OH group of a ribonucleotide may be replaced by 2'-F or 2'-NH<sub>2</sub>), which may improve a desired property, e.g., resistance to nucleases or longer lifetime in blood. Aptamers may be conjugated to other molecules, e.g., a high molecular weight carrier to slow clearance of the aptamer from the circulatory system.

Aptamers may be specifically cross-linked to their cognate ligands, e.g., by photo-activation of a cross-linker. (See, e.g., Brody, E.N. and L. Gold (2000) J. Biotechnol. 74:5-13.)

The term "intramer" refers to an aptamer which is expressed in vivo. For example, a vaccinia virus-based RNA expression system has been used to express specific RNA aptamers at high levels  
5 in the cytoplasm of leukocytes (Blind, M. et al. (1999) Proc. Natl Acad. Sci. USA 96:3606-3610).

The term "spiegelmer" refers to an aptamer which includes L-DNA, L-RNA, or other left-handed nucleotide derivatives or nucleotide-like molecules. Aptamers containing left-handed nucleotides are resistant to degradation by naturally occurring enzymes, which normally act on substrates containing right-handed nucleotides.

10 "Antisense sequence" refers to a sequence capable of specifically hybridizing to a target sequence. The antisense sequence may include DNA, RNA, or any nucleic acid mimic or analog such as peptide nucleic acid (PNA); oligonucleotides having modified backbone linkages such as phosphorothioates, methylphosphonates, or benzylphosphonates; oligonucleotides having modified sugar groups such as 2'-methoxyethyl sugars or 2'-methoxyethoxy sugars; or oligonucleotides having  
15 modified bases such as 5-methyl cytosine, 2'-deoxyuracil, or 7-deaza-2'-deoxyguanosine.

"Antisense technology" refers to any technology which relies on the specific hybridization of an antisense sequence to a target sequence.

A "bin" is a portion of computer memory space used by a computer program for storage of data, and bounded in such a manner that data stored in a bin may be retrieved by the program.

20 "Biologically active" refers to an amino acid sequence having a structural, regulatory, or biochemical function of a naturally occurring amino acid sequence.

"Clone joining" is a process for combining gene bins based upon the bins' containing sequence information from the same clone. The sequences may assemble into a primary gene transcript as well as one or more splice variants.

25 "Complementary" describes the relationship between two single-stranded nucleic acid sequences that anneal by base-pairing (5'-A-G-T-3' pairs with its complement 3'-T-C-A-5').

A "component sequence" is a nucleic acid sequence selected by a computer program such as PHRED and used to assemble a consensus or template sequence from one or more component sequences.

30 A "consensus sequence" or "template sequence" is a nucleic acid sequence which has been assembled from overlapping sequences, using a computer program for fragment assembly such as the GELVIEW fragment assembly system (Genetics Computer Group (GCG), Madison WI) or using a relational database management system (RDMS).

"Conservative amino acid substitutions" are those substitutions that, when made, least  
35 interfere with the properties of the original protein, i.e., the structure and especially the function of the

protein is conserved and not significantly changed by such substitutions. The table below shows amino acids which may be substituted for an original amino acid in a protein and which are regarded as conservative substitutions.

5	<b>Original Residue</b>	<b>Conservative Substitution</b>
	Ala	Gly, Ser
	Arg	His, Lys
	Asn	Asp, Gln, His
	Asp	Asn, Glu
10	Cys	Ala, Ser
	Gln	Asn, Glu, His
	Glu	Asp, Gln, His
	Gly	Ala
	His	Asn, Arg, Gln, Glu
15	Ile	Leu, Val
	Leu	Ile, Val
	Lys	Arg, Gln, Glu
	Met	Leu, Ile
	Phe	His, Met, Leu, Trp, Tyr
20	Ser	Cys, Thr
	Thr	Ser, Val
	Trp	Phe, Tyr
	Tyr	His, Phe, Trp
25	Val	Ile, Leu, Thr

Conservative substitutions generally maintain (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a beta sheet or alpha helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain.

30 “Deletion” refers to a change in either a nucleic or amino acid sequence in which at least one nucleotide or amino acid residue, respectively, is absent.

“Derivative” refers to the chemical modification of a nucleic acid sequence, such as by replacement of hydrogen by an alkyl, acyl, amino, hydroxyl, or other group.

35 “Differential expression” refers to increased or upregulated; or decreased, downregulated, or absent gene or protein expression, determined by comparing at least two different samples. Such comparisons may be carried out between, for example, a treated and an untreated sample, or a diseased and a normal sample.

The terms “element” and “array element” refer to a polynucleotide, polypeptide, or other chemical compound having a unique and defined position on a microarray.

The term "modulate" refers to a change in the activity of MDDT. For example, modulation may cause an increase or a decrease in protein activity, binding characteristics, or any other biological, functional, or immunological properties of MDDT.

"E-value" refers to the statistical probability that a match between two sequences occurred by  
5 chance.

"Exon shuffling" refers to the recombination of different coding regions (exons). Since an exon may represent a structural or functional domain of the encoded protein, new proteins may be assembled through the novel reassortment of stable substructures, thus allowing acceleration of the evolution of new protein functions.

10 A "fragment" is a unique portion of mddt or MDDT which is identical in sequence to but shorter in length than the parent sequence. A fragment may comprise up to the entire length of the defined sequence, minus one nucleotide/amino acid residue. For example, a fragment may comprise from 10 to 1000 contiguous amino acid residues or nucleotides. A fragment used as a probe, primer, antigen, therapeutic molecule, or for other purposes, may be at least 5, 10, 15, 16, 20, 25, 30, 40, 50, 60,  
15 75, 100, 150, 250 or at least 500 contiguous amino acid residues or nucleotides in length. Fragments may be preferentially selected from certain regions of a molecule. For example, a polypeptide fragment may comprise a certain length of contiguous amino acids selected from the first 250 or 500 amino acids (or first 25% or 50%) of a polypeptide as shown in a certain defined sequence. Clearly these lengths are exemplary, and any length that is supported by the specification, including the  
20 Sequence Listing and the figures, may be encompassed by the present embodiments.

A fragment of mddt comprises a region of unique polynucleotide sequence that specifically identifies mddt, for example, as distinct from any other sequence in the same genome. A fragment of mddt is useful, for example, in hybridization and amplification technologies and in analogous methods that distinguish mddt from related polynucleotide sequences. The precise length of a fragment of mddt  
25 and the region of mddt to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

A fragment of MDDT is encoded by a fragment of mddt. A fragment of MDDT comprises a region of unique amino acid sequence that specifically identifies MDDT. For example, a fragment of MDDT is useful as an immunogenic peptide for the development of antibodies that specifically  
30 recognize MDDT. The precise length of a fragment of MDDT and the region of MDDT to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

A "full length" nucleotide sequence is one containing at least a start site for translation to a protein sequence, followed by an open reading frame and a stop site, and encoding a "full length"  
35 polypeptide.

“Hit” refers to a sequence whose annotation will be used to describe a given template.

Criteria for selecting the top hit are as follows: if the template has one or more exact nucleic acid matches, the top hit is the exact match with highest percent identity. If the template has no exact matches but has significant protein hits, the top hit is the protein hit with the lowest E-value. If the  
5 template has no significant protein hits, but does have significant non-exact nucleotide hits, the top hit is the nucleotide hit with the lowest E-value.

“Homology” refers to sequence similarity either between a reference nucleic acid sequence and at least a fragment of an mddt or between a reference amino acid sequence and a fragment of an MDDT.

10 “Hybridization” refers to the process by which a strand of nucleotides anneals with a complementary strand through base pairing. Specific hybridization is an indication that two nucleic acid sequences share a high degree of identity. Specific hybridization complexes form under defined annealing conditions, and remain hybridized after the “washing” step. The defined hybridization conditions include the annealing conditions and the washing step(s), the latter of which is particularly  
15 important in determining the stringency of the hybridization process, with more stringent conditions allowing less non-specific binding, i.e., binding between pairs of nucleic acid probes that are not perfectly matched. Permissive conditions for annealing of nucleic acid sequences are routinely determinable and may be consistent among hybridization experiments, whereas wash conditions may be varied among experiments to achieve the desired stringency.

20 Generally, stringency of hybridization is expressed with reference to the temperature under which the wash step is carried out. Generally, such wash temperatures are selected to be about 5°C to 20°C lower than the thermal melting point ( $T_m$ ) for the specific sequence at a defined ionic strength and pH. The  $T_m$  is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. An equation for calculating  $T_m$  and conditions for  
25 nucleic acid hybridization is well known and can be found in Sambrook et al., 1989, Molecular Cloning: A Laboratory Manual, 2<sup>nd</sup> ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; specifically see volume 2, chapter 9.

High stringency conditions for hybridization between polynucleotides of the present invention include wash conditions of 68°C in the presence of about 0.2 x SSC and about 0.1% SDS, for 1 hour.  
30 Alternatively, temperatures of about 65°C, 60°C, or 55°C may be used. SSC concentration may be varied from about 0.2 to 2 x SSC, with SDS being present at about 0.1%. Typically, blocking reagents are used to block non-specific hybridization. Such blocking reagents include, for instance, denatured salmon sperm DNA at about 100-200 µg/ml. Useful variations on these conditions will be readily apparent to those skilled in the art. Hybridization, particularly under high stringency conditions, may be  
35 suggestive of evolutionary similarity between the nucleotides. Such similarity is strongly indicative of a

similar role for the nucleotides and their resultant proteins.

Other parameters, such as temperature, salt concentration, and detergent concentration may be varied to achieve the desired stringency. Denaturants, such as formamide at a concentration of about 35-50% v/v, may also be used under particular circumstances, such as RNA:DNA

5 hybridizations. Appropriate hybridization conditions are routinely determinable by one of ordinary skill in the art.

"Immunologically active" or "immunogenic" describes the potential for a natural, recombinant, or synthetic peptide, epitope, polypeptide, or protein to induce antibody production in appropriate animals, cells, or cell lines.

10 "Immune response" can refer to conditions associated with inflammation, trauma, immune disorders, or infectious or genetic disease, etc. These conditions can be characterized by expression of various factors, e.g., cytokines, chemokines, and other signaling molecules, which may affect cellular and systemic defense systems.

An "immunogenic fragment" is a polypeptide or oligopeptide fragment of ABBR which is  
15 capable of eliciting an immune response when introduced into a living organism, for example, a mammal. The term "immunogenic fragment" also includes any polypeptide or oligopeptide fragment of ABBR which is useful in any of the antibody production methods disclosed herein or known in the art.

"Insertion" or "addition" refers to a change in either a nucleic or amino acid sequence in  
20 which at least one nucleotide or residue, respectively, is added to the sequence.

"Labeling" refers to the covalent or noncovalent joining of a polynucleotide, polypeptide, or antibody with a reporter molecule capable of producing a detectable or measurable signal.

"Microarray" is any arrangement of nucleic acids, amino acids, antibodies, etc., on a substrate. The substrate may be a solid support such as beads, glass, paper, nitrocellulose, nylon, or an  
25 appropriate membrane.

"Linkers" are short stretches of nucleotide sequence which may be added to a vector or an mddt to create restriction endonuclease sites to facilitate cloning. "Polylinkers" are engineered to incorporate multiple restriction enzyme sites and to provide for the use of enzymes which leave 5' or 3' overhangs (e.g., BamHI, EcoRI, and HindIII) and those which provide blunt ends (e.g., EcoRV,  
30 SnaBI, and StuI).

"Naturally occurring" refers to an endogenous polynucleotide or polypeptide that may be isolated from viruses or prokaryotic or eukaryotic cells.

"Nucleic acid sequence" refers to the specific order of nucleotides joined by phosphodiester bonds in a linear, polymeric arrangement. Depending on the number of nucleotides, the nucleic acid  
35 sequence can be considered an oligomer, oligonucleotide, or polynucleotide. The nucleic acid can be

DNA, RNA, or any nucleic acid analog, such as PNA, may be of genomic or synthetic origin, may be either double-stranded or single-stranded, and can represent either the sense or antisense (complementary) strand.

“Oligomer” refers to a nucleic acid sequence of at least about 6 nucleotides and as many as about 60 nucleotides, preferably about 15 to 40 nucleotides, and most preferably between about 20 and 30 nucleotides, that may be used in hybridization or amplification technologies. Oligomers may be used as, e.g., primers for PCR, and are usually chemically synthesized.

“Operably linked” refers to the situation in which a first nucleic acid sequence is placed in a functional relationship with the second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. Generally, operably linked DNA sequences may be in close proximity or contiguous and, where necessary to join two protein coding regions, in the same reading frame.

“Peptide nucleic acid” (PNA) refers to a DNA mimic in which nucleotide bases are attached to a pseudopeptide backbone to increase stability. PNAs, also designated antigene agents, can prevent gene expression by targeting complementary messenger RNA.

The phrases “percent identity” and “% identity”, as applied to polynucleotide sequences, refer to the percentage of residue matches between at least two polynucleotide sequences aligned using a standardized algorithm. Such an algorithm may insert, in a standardized and reproducible way, gaps in the sequences being compared in order to optimize alignment between two sequences, and therefore achieve a more meaningful comparison of the two sequences.

Percent identity between polynucleotide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program. This program is part of the LASERGENE software package, a suite of molecular biological analysis programs (DNASTAR, Madison WI). CLUSTAL V is described in Higgins, D.G. and Sharp, P.M. (1989) CABIOS 5:151-153 and in Higgins, D.G. et al. (1992) CABIOS 8:189-191. For pairwise alignments of polynucleotide sequences, the default parameters are set as follows: Ktuple=2, gap penalty=5, window=4, and “diagonals saved”=4. The “weighted” residue weight table is selected as the default. Percent identity is reported by CLUSTAL V as the “percent similarity” between aligned polynucleotide sequence pairs.

Alternatively, a suite of commonly used and freely available sequence comparison algorithms is provided by the National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST) (Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410), which is available from several sources, including the NCBI, Bethesda, MD, and on the Internet at <http://www.ncbi.nlm.nih.gov/BLAST/>. The BLAST software suite includes various sequence analysis programs including “BLASTN,” that is used to determine alignment between a known polynucleotide

sequence and other sequences on a variety of databases. Also available is a tool called "BLAST 2 Sequences" that is used for direct pairwise comparison of two nucleotide sequences. "BLAST 2 Sequences" can be accessed and used interactively at <http://www.ncbi.nlm.nih.gov/gorf/bl2/>. The "BLAST 2 Sequences" tool can be used for both BLASTN and BLASTP (discussed below).

- 5 BLAST programs are commonly used with gap and other parameters set to default settings. For example, to compare two nucleotide sequences, one may use BLASTN with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such default parameters may be, for example:

*Matrix: BLOSUM62*

10 *Reward for match: 1*

*Penalty for mismatch: -2*

*Open Gap: 5 and Extension Gap: 2 penalties*

*Gap x drop-off: 50*

*Expect: 10*

15 *Word Size: 11*

*Filter: on*

- Percent identity may be measured over the length of an entire defined sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined sequence, for instance, a fragment of at  
20 least 20, at least 30, at least 40, at least 50, at least 70, at least 100, or at least 200 contiguous nucleotides. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in figures or Sequence Listings, may be used to describe a length over which percentage identity may be measured.

- Nucleic acid sequences that do not show a high degree of identity may nevertheless encode  
25 similar amino acid sequences due to the degeneracy of the genetic code. It is understood that changes in nucleic acid sequence can be made using this degeneracy to produce multiple nucleic acid sequences that all encode substantially the same protein.

- The phrases "percent identity" and "% identity", as applied to polypeptide sequences, refer to the percentage of residue matches between at least two polypeptide sequences aligned using a  
30 standardized algorithm. Methods of polypeptide sequence alignment are well-known. Some alignment methods take into account conservative amino acid substitutions. Such conservative substitutions, explained in more detail above, generally preserve the hydrophobicity and acidity of the substituted residue, thus preserving the structure (and therefore function) of the folded polypeptide.

- Percent identity between polypeptide sequences may be determined using the default  
35 parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e



sequence alignment program (described and referenced above). For pairwise alignments of polypeptide sequences using CLUSTAL V, the default parameters are set as follows: Ktuple=1, gap penalty=3, window=5, and "diagonals saved"=5. The PAM250 matrix is selected as the default residue weight table. As with polynucleotide alignments, the percent identity is reported by  
5 CLUSTAL V as the "percent similarity" between aligned polypeptide sequence pairs.

Alternatively the NCBI BLAST software suite may be used. For example, for a pairwise comparison of two polypeptide sequences, one may use the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) with BLASTP set at default parameters. Such default parameters may be, for example:

10        *Matrix: BLOSUM62*  
         *Open Gap: 11 and Extension Gap: 1 penalty*  
         *Gap x drop-off: 50*  
         *Expect: 10*  
         *Word Size: 3*  
15        *Filter: on*

Percent identity may be measured over the length of an entire defined polypeptide sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined polypeptide sequence, for instance, a fragment of at least 15, at least 20, at least 30, at least 40, at least 50, at least 70 or at least  
20 150 contiguous residues. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in figures or Sequence Listings, may be used to describe a length over which percentage identity may be measured.

"Post-translational modification" of an MDDT may involve lipidation, glycosylation, phosphorylation, acetylation, racemization, proteolytic cleavage, and other modifications known in the  
25 art. These processes may occur synthetically or biochemically. Biochemical modifications will vary by cell type depending on the enzymatic milieu and the MDDT.

"Probe" refers to mddt or fragments thereof, which are used to detect identical, allelic or related nucleic acid sequences. Probes are isolated oligonucleotides or polynucleotides attached to a detectable label or reporter molecule. Typical labels include radioactive isotopes, ligands,  
30 chemiluminescent agents, and enzymes. "Primers" are short nucleic acids, usually DNA oligonucleotides, which may be annealed to a target polynucleotide by complementary base-pairing. The primer may then be extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification (and identification) of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR).

35        Probes and primers as used in the present invention typically comprise at least 15 contiguous

nucleotides of a known sequence. In order to enhance specificity, longer probes and primers may also be employed, such as probes and primers that comprise at least 20, 30, 40, 50, 60, 70, 80, 90, 100, or at least 150 consecutive nucleotides of the disclosed nucleic acid sequences. Probes and primers may be considerably longer than these examples, and it is understood that any length supported by the specification, including the figures and Sequence Listing, may be used.

Methods for preparing and using probes and primers are described in the references, for example Sambrook et al., 1989, Molecular Cloning: A Laboratory Manual, 2<sup>nd</sup> ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; Ausubel et al., 1987, Current Protocols in Molecular Biology, Greene Publ. Assoc. & Wiley-Intersciences, New York NY; Innis et al., 1990, PCR Protocols, A Guide to Methods and Applications, Academic Press, San Diego CA. PCR primer pairs can be derived from a known sequence, for example, by using computer programs intended for that purpose such as Primer (Version 0.5, 1991, Whitehead Institute for Biomedical Research, Cambridge MA).

Oligonucleotides for use as primers are selected using software known in the art for such purpose. For example, OLIGO 4.06 software is useful for the selection of PCR primer pairs of up to 100 nucleotides each, and for the analysis of oligonucleotides and larger polynucleotides of up to 5,000 nucleotides from an input polynucleotide sequence of up to 32 kilobases. Similar primer selection programs have incorporated additional features for expanded capabilities. For example, the PrimOU primer selection program (available to the public from the Genome Center at University of Texas South West Medical Center, Dallas TX) is capable of choosing specific primers from megabase sequences and is thus useful for designing primers on a genome-wide scope. The Primer3 primer selection program (available to the public from the Whitehead Institute/MIT Center for Genome Research, Cambridge MA) allows the user to input a "mispriming library," in which sequences to avoid as primer binding sites are user-specified. Primer3 is useful, in particular, for the selection of oligonucleotides for microarrays. (The source code for the latter two primer selection programs may also be obtained from their respective sources and modified to meet the user's specific needs.) The PrimeGen program (available to the public from the UK Human Genome Mapping Project Resource Centre, Cambridge UK) designs primers based on multiple sequence alignments, thereby allowing selection of primers that hybridize to either the most conserved or least conserved regions of aligned nucleic acid sequences. Hence, this program is useful for identification of both unique and conserved oligonucleotides and polynucleotide fragments. The oligonucleotides and polynucleotide fragments identified by any of the above selection methods are useful in hybridization technologies, for example, as PCR or sequencing primers, microarray elements, or specific probes to identify fully or partially complementary polynucleotides in a sample of nucleic acids. Methods of oligonucleotide selection are not limited to those described above.

"Purified" refers to molecules, either polynucleotides or polypeptides that are isolated or

separated from their natural environment and are at least 60% free, preferably at least 75% free, and most preferably at least 90% free from other compounds with which they are naturally associated.

A "recombinant nucleic acid" is a sequence that is not naturally occurring or has a sequence that is made by an artificial combination of two or more otherwise separated segments of sequence.

5 This artificial combination is often accomplished by chemical synthesis or, more commonly, by the artificial manipulation of isolated segments of nucleic acids, e.g., by genetic engineering techniques such as those described in Sambrook, supra. The term recombinant includes nucleic acids that have been altered solely by addition, substitution, or deletion of a portion of the nucleic acid. Frequently, a recombinant nucleic acid may include a nucleic acid sequence operably linked to a promoter sequence.  
10 Such a recombinant nucleic acid may be part of a vector that is used, for example, to transform a cell.

Alternatively, such recombinant nucleic acids may be part of a viral vector, e.g., based on a vaccinia virus, that could be used to vaccinate a mammal wherein the recombinant nucleic acid is expressed, inducing a protective immunological response in the mammal.

"Regulatory element" refers to a nucleic acid sequence from nontranslated regions of a gene,  
15 and includes enhancers, promoters, introns, and 3' untranslated regions, which interact with host proteins to carry out or regulate transcription or translation.

"Reporter" molecules are chemical or biochemical moieties used for labeling a nucleic acid, an amino acid, or an antibody. They include radionuclides; enzymes; fluorescent, chemiluminescent, or chromogenic agents; substrates; cofactors; inhibitors; magnetic particles; and other moieties known in  
20 the art.

An "RNA equivalent," in reference to a DNA sequence, is composed of the same linear sequence of nucleotides as the reference DNA sequence with the exception that all occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose instead of deoxyribose.

25 "Sample" is used in its broadest sense. Samples may contain nucleic or amino acids, antibodies, or other materials, and may be derived from any source (e.g., bodily fluids including, but not limited to, saliva, blood, and urine; chromosome(s), organelles, or membranes isolated from a cell; genomic DNA, RNA, or cDNA in solution or bound to a substrate; and cleared cells or tissues or blots or imprints from such cells or tissues).

30 "Specific binding" or "specifically binding" refers to the interaction between a protein or peptide and its agonist, antibody, antagonist, or other binding partner. The interaction is dependent upon the presence of a particular structure of the protein, e.g., the antigenic determinant or epitope, recognized by the binding molecule. For example, if an antibody is specific for epitope "A," the presence of a polypeptide containing epitope A, or the presence of free unlabeled A, in a reaction

containing free labeled A and the antibody will reduce the amount of labeled A that binds to the antibody.

"Substitution" refers to the replacement of at least one nucleotide or amino acid by a different nucleotide or amino acid.

5 "Substrate" refers to any suitable rigid or semi-rigid support including, e.g., membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, tubing, plates, polymers, microparticles or capillaries. The substrate can have a variety of surface forms, such as wells, trenches, pins, channels and pores, to which polynucleotides or polypeptides are bound.

A "transcript image" refers to the collective pattern of gene expression by a particular tissue  
10 or cell type under given conditions at a given time.

"Transformation" refers to a process by which exogenous DNA enters a recipient cell. Transformation may occur under natural or artificial conditions using various methods well known in the art. Transformation may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method is selected based on the host cell  
15 being transformed.

"Transformants" include stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome, as well as cells which transiently express inserted DNA or RNA.

A "transgenic organism," as used herein, is any organism, including but not limited to animals  
20 and plants, in which one or more of the cells of the organism contains heterologous nucleic acid introduced by way of human intervention, such as by transgenic techniques well known in the art. The nucleic acid is introduced into the cell, directly or indirectly by introduction into a precursor of the cell, by way of deliberate genetic manipulation, such as by microinjection or by infection with a recombinant virus. The term genetic manipulation does not include classical cross-breeding, or in vitro  
25 fertilization, but rather is directed to the introduction of a recombinant DNA molecule. The transgenic organisms contemplated in accordance with the present invention include bacteria, cyanobacteria, fungi, and plants and animals. The isolated DNA of the present invention can be introduced into the host by methods known in the art, for example infection, transfection, transformation or transconjugation. Techniques for transferring the DNA of the present invention into such organisms  
30 are widely known and provided in references such as Sambrook et al. (1989), supra.

A "variant" of a particular nucleic acid sequence is defined as a nucleic acid sequence having at least 25% sequence identity to the particular nucleic acid sequence over a certain length of one of the nucleic acid sequences using BLASTN with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of nucleic acids may show, for example, at least 30%,  
35 at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 91%, at least 92%, at

least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% or greater sequence identity over a certain defined length. The variant may result in "conservative" amino acid changes which do not affect structural and/or chemical properties. A variant may be described as, for example, an "allelic" (as defined above), "splice," "species," or "polymorphic" variant. A splice variant may have significant identity to a reference molecule, but will generally have a greater or lesser number of polynucleotides due to alternate splicing of exons during mRNA processing. The corresponding polypeptide may possess additional functional domains or lack domains that are present in the reference molecule. Species variants are polynucleotide sequences that vary from one species to another. The resulting polypeptides generally will have significant amino acid identity relative to each other. A polymorphic variant is a variation in the polynucleotide sequence of a particular gene between individuals of a given species. Polymorphic variants also may encompass "single nucleotide polymorphisms" (SNPs) in which the polynucleotide sequence varies by one base. The presence of SNPs may be indicative of, for example, a certain population, a disease state, or a propensity for a disease state.

In an alternative, variants of the polynucleotides of the present invention may be generated through recombinant methods. One possible method is a DNA shuffling technique such as MOLECULARBREEDING (Maxygen Inc., Santa Clara CA; described in U.S. Patent Number 5,837,458; Chang, C.-C. et al. (1999) Nat. Biotechnol. 17:793-797; Christians, F.C. et al. (1999) Nat. Biotechnol. 17:259-264; and Cramer, A. et al. (1996) Nat. Biotechnol. 14:315-319) to alter or improve the biological properties of MDDT, such as its biological or enzymatic activity or its ability to bind to other molecules or compounds. DNA shuffling is a process by which a library of gene variants is produced using PCR-mediated recombination of gene fragments. The library is then subjected to selection or screening procedures that identify those gene variants with the desired properties. These preferred variants may then be pooled and further subjected to recursive rounds of DNA shuffling and selection/screening. Thus, genetic diversity is created through "artificial" breeding and rapid molecular evolution. For example, fragments of a single gene containing random point mutations may be recombined, screened, and then reshuffled until the desired properties are optimized. Alternatively, fragments of a given gene may be recombined with fragments of homologous genes in the same gene family, either from the same or different species, thereby maximizing the genetic diversity of multiple naturally occurring genes in a directed and controllable manner.

A "variant" of a particular polypeptide sequence is defined as a polypeptide sequence having at least 40% sequence identity to the particular polypeptide sequence over a certain length of one of the polypeptide sequences using BLASTP with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of polypeptides may show, for example, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at

least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% or greater sequence identity over a certain defined length of one of the polypeptides.

## THE INVENTION

5 In a particular embodiment, cDNA sequences derived from human tissues and cell lines were aligned based on nucleotide sequence identity and assembled into "consensus" or "template" sequences which are designated by the template identification numbers (template IDs) in column 2 of Table 2. The sequence identification numbers (SEQ ID NO:s) corresponding to the template IDs are shown in column 1. The template sequences have similarity to GenBank sequences, or "hits," as  
10 designated by the GI Numbers in column 3. The statistical probability of each GenBank hit is indicated by a probability score in column 4, and the functional annotation corresponding to each GenBank hit is listed in column 5.

The invention incorporates the nucleic acid sequences of these templates as disclosed in the Sequence Listing and the use of these sequences in the diagnosis and treatment of disease states  
15 characterized by defects in disease detection and treatment molecules. The invention further utilizes these sequences in hybridization and amplification technologies, and in particular, in technologies which assess gene expression patterns correlated with specific cells or tissues and their responses in vivo or in vitro to pharmaceutical agents, toxins, and other treatments. In this manner, the sequences of the present invention are used to develop a transcript image for a particular cell or tissue.

20

### Derivation of Nucleic Acid Sequences

cDNA was isolated from libraries constructed using RNA derived from normal and diseased human tissues and cell lines. The human tissues and cell lines used for cDNA library construction were selected from a broad range of sources to provide a diverse population of cDNAs representative  
25 of gene transcription throughout the human body. Descriptions of the human tissues and cell lines used for cDNA library construction are provided in the LIFESEQ database (Incyte Genomics, Inc. (Incyte), Palo Alto CA). Human tissues were broadly selected from, for example, cardiovascular, dermatologic, endocrine, gastrointestinal, hematopoietic/immune system, musculoskeletal, neural, reproductive, and urologic sources.

30 Cell lines used for cDNA library construction were derived from, for example, leukemic cells, teratocarcinomas, neuroepitheliomas, cervical carcinoma, lung fibroblasts, and endothelial cells. Such cell lines include, for example, THP-1, Jurkat, HUVEC, hNT2, WI38, HeLa, and other cell lines commonly used and available from public depositories (American Type Culture Collection, Manassas VA). Prior to mRNA isolation, cell lines were untreated, treated with a pharmaceutical agent such as

5'-aza-2'-deoxycytidine, treated with an activating agent such as lipopolysaccharide in the case of leukocytic cell lines, or, in the case of endothelial cell lines, subjected to shear stress.

### Sequencing of the cDNAs

5           Methods for DNA sequencing are well known in the art. Conventional enzymatic methods employ the Klenow fragment of DNA polymerase I, SEQUENASE DNA polymerase (U.S. Biochemical Corporation, Cleveland OH), Taq polymerase (Applied Biosystems, Foster City CA), thermostable T7 polymerase (Amersham Pharmacia Biotech, Inc. (Amersham Pharmacia Biotech), Piscataway NJ), or combinations of polymerases and proofreading exonucleases such as those found  
10   in the ELONGASE amplification system (Life Technologies Inc. (Life Technologies), Gaithersburg MD), to extend the nucleic acid sequence from an oligonucleotide primer annealed to the DNA template of interest. Methods have been developed for the use of both single-stranded and double-stranded templates. Chain termination reaction products may be electrophoresed on urea-polyacrylamide gels and detected either by autoradiography (for radioisotope-labeled nucleotides) or  
15   by fluorescence (for fluorophore-labeled nucleotides). Automated methods for mechanized reaction preparation, sequencing, and analysis using fluorescence detection methods have been developed. Machines used to prepare cDNAs for sequencing can include the MICROLAB 2200 liquid transfer system (Hamilton Company (Hamilton), Reno NV), Peltier thermal cycler (PTC200; MJ Research, Inc. (MJ Research), Watertown MA), and ABI CATALYST 800 thermal cycler (Applied  
20   Biosystems). Sequencing can be carried out using, for example, the ABI 373 or 377 (Applied Biosystems) or MEGABACE 1000 (Molecular Dynamics, Inc. (Molecular Dynamics), Sunnyvale CA) DNA sequencing systems, or other automated and manual sequencing systems well known in the art.

          The nucleotide sequences of the Sequence Listing have been prepared by current, state-of-  
25   the-art, automated methods and, as such, may contain occasional sequencing errors or unidentified nucleotides. Such unidentified nucleotides are designated by an N. These infrequent unidentified bases do not represent a hindrance to practicing the invention for those skilled in the art. Several methods employing standard recombinant techniques may be used to correct errors and complete the missing sequence information. (See, e.g., those described in Ausubel, F.M. et al. (1997) Short  
30   Protocols in Molecular Biology, John Wiley & Sons, New York NY; and Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview NY.)

### Assembly of cDNA Sequences

          Human polynucleotide sequences may be assembled using programs or algorithms well known  
35   in the art. Sequences to be assembled are related, wholly or in part, and may be derived from a single

or many different transcripts. Assembly of the sequences can be performed using such programs as PHRAP (Phils Revised Assembly Program) and the GELVIEW fragment assembly system (GCG), or other methods known in the art.

Alternatively, cDNA sequences are used as "component" sequences that are assembled into "template" or "consensus" sequences as follows. Sequence chromatograms are processed, verified, and quality scores are obtained using PHRED. Raw sequences are edited using an editing pathway known as Block 1 (See, e.g., the LIFESEQ Assembled User Guide, Incyte Genomics, Palo Alto, CA). A series of BLAST comparisons is performed and low-information segments and repetitive elements (e.g., dinucleotide repeats, Alu repeats, etc.) are replaced by "n's", or masked, to prevent spurious matches. Mitochondrial and ribosomal RNA sequences are also removed. The processed sequences are then loaded into a relational database management system (RDMS) which assigns edited sequences to existing templates, if available. When additional sequences are added into the RDMS, a process is initiated which modifies existing templates or creates new templates from works in progress (i.e., nonfinal assembled sequences) containing queued sequences or the sequences themselves. After the new sequences have been assigned to templates, the templates can be merged into bins. If multiple templates exist in one bin, the bin can be split and the templates reannotated.

Once gene bins have been generated based upon sequence alignments, bins are "clone joined" based upon clone information. Clone joining occurs when the 5' sequence of one clone is present in one bin and the 3' sequence from the same clone is present in a different bin, indicating that the two bins should be merged into a single bin. Only bins which share at least two different clones are merged.

A resultant template sequence may contain either a partial or a full length open reading frame, or all or part of a genetic regulatory element. This variation is due in part to the fact that the full length cDNAs of many genes are several hundred, and sometimes several thousand, bases in length. With current technology, cDNAs comprising the coding regions of large genes cannot be cloned because of vector limitations, incomplete reverse transcription of the mRNA, or incomplete "second strand" synthesis. Template sequences may be extended to include additional contiguous sequences derived from the parent RNA transcript using a variety of methods known to those of skill in the art. Extension may thus be used to achieve the full length coding sequence of a gene.

### Analysis of the cDNA Sequences

The cDNA sequences are analyzed using a variety of programs and algorithms which are well known in the art. (See, e.g., Ausubel, 1997, supra, Chapter 7.7; Meyers, R.A. (Ed.) (1995) Molecular Biology and Biotechnology, Wiley VCH, New York NY, pp. 856-853; and Table 8.) These analyses comprise both reading frame determinations, e.g., based on triplet codon periodicity for



particular organisms (Fickett, J.W. (1982) *Nucleic Acids Res.* 10:5303-5318); analyses of potential start and stop codons; and homology searches.

Computer programs known to those of skill in the art for performing computer-assisted searches for amino acid and nucleic acid sequence similarity, include, for example, Basic Local Alignment Search Tool (BLAST; Altschul, S.F. (1993) *J. Mol. Evol.* 36:290-300; Altschul, S.F. et al. (1990) *J. Mol. Biol.* 215:403-410). BLAST is especially useful in determining exact matches and comparing two sequence fragments of arbitrary but equal lengths, whose alignment is locally maximal and for which the alignment score meets or exceeds a threshold or cutoff score set by the user (Karlin, S. et al. (1988) *Proc. Natl. Acad. Sci. USA* 85:841-845). Using an appropriate search tool (e.g., BLAST or HMM), GenBank, SwissProt, BLOCKS, PFAM and other databases may be searched for sequences containing regions of homology to a query mddt or MDDT of the present invention.

Other approaches to the identification, assembly, storage, and display of nucleotide and polypeptide sequences are provided in "Relational Database for Storing Biomolecule Information," U.S.S.N. 08/947,845, filed October 9, 1997; "Project-Based Full-Length Biomolecular Sequence Database," U.S. Patent Number 5,953,727; and "Relational Database and System for Storing Information Relating to Biomolecular Sequences," U.S.S.N. 09/034,807, filed March 4, 1998, all of which are incorporated by reference herein in their entirety.

Protein hierarchies can be assigned to the putative encoded polypeptide based on, e.g., motif, BLAST, or biological analysis. Methods for assigning these hierarchies are described, for example, in "Database System Employing Protein Function Hierarchies for Viewing Biomolecular Sequence Data," U.S. Patent Number 6,023,659, incorporated herein by reference.

#### Human Disease Detection and Treatment Molecule Sequences

The mddt of the present invention may be used for a variety of diagnostic and therapeutic purposes. For example, an mddt may be used to diagnose a particular condition, disease, or disorder associated with disease detection and treatment molecules. Such conditions, diseases, and disorders include, but are not limited to, a cell proliferative disorder, such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, a cancer of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus; and an autoimmune/inflammatory disorder, such as actinic keratosis, acquired immunodeficiency

syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, arteriosclerosis, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, bronchitis, bursitis, cholecystitis, cirrhosis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, paroxysmal nocturnal hemoglobinuria, hepatitis, hypereosinophilia, irritable bowel syndrome, episodic lymphopenia with lymphocytotoxins, mixed connective tissue disease (MCTD), multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, myelofibrosis, osteoarthritis, osteoporosis, pancreatitis, polycythemia vera, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, primary thrombocythemia, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, trauma, and hematopoietic cancer including lymphoma, leukemia, and myeloma. The mddt can be used to detect the presence of, or to quantify the amount of, an mddt-related polynucleotide in a sample. This information is then compared to information obtained from appropriate reference samples, and a diagnosis is established. Alternatively, a polynucleotide complementary to a given mddt can inhibit or inactivate a therapeutically relevant gene related to the mddt.

#### 20 Analysis of mddt Expression Patterns

The expression of mddt may be routinely assessed by hybridization-based methods to determine, for example, the tissue-specificity, disease-specificity, or developmental stage-specificity of mddt expression. For example, the level of expression of mddt may be compared among different cell types or tissues, among diseased and normal cell types or tissues, among cell types or tissues at different developmental stages, or among cell types or tissues undergoing various treatments. This type of analysis is useful, for example, to assess the relative levels of mddt expression in fully or partially differentiated cells or tissues, to determine if changes in mddt expression levels are correlated with the development or progression of specific disease states, and to assess the response of a cell or tissue to a specific therapy, for example, in pharmacological or toxicological studies. Methods for the analysis of mddt expression are based on hybridization and amplification technologies and include membrane-based procedures such as northern blot analysis, high-throughput procedures that utilize, for example, microarrays, and PCR-based procedures.

#### Hybridization and Genetic Analysis

35 The mddt, their fragments, or complementary sequences, may be used to identify the presence

of and/or to determine the degree of similarity between two (or more) nucleic acid sequences. The mddt may be hybridized to naturally occurring or recombinant nucleic acid sequences under appropriately selected temperatures and salt concentrations. Hybridization with a probe based on the nucleic acid sequence of at least one of the mddt allows for the detection of nucleic acid sequences, including genomic sequences, which are identical or related to the mddt of the Sequence Listing. Probes may be selected from non-conserved or unique regions of at least one of the polynucleotides of SEQ ID NO:1-396 and tested for their ability to identify or amplify the target nucleic acid sequence using standard protocols.

Polynucleotide sequences that are capable of hybridizing, in particular, to those shown in SEQ ID NO:1-396 and fragments thereof, can be identified using various conditions of stringency. (See, e.g., Wahl, G.M. and S.L. Berger (1987) *Methods Enzymol.* 152:399-407; Kimmel, A.R. (1987) *Methods Enzymol.* 152:507-511.) Hybridization conditions are discussed in "Definitions."

A probe for use in Southern or northern hybridization may be derived from a fragment of an mddt sequence, or its complement, that is up to several hundred nucleotides in length and is either single-stranded or double-stranded. Such probes may be hybridized in solution to biological materials such as plasmids, bacterial, yeast, or human artificial chromosomes, cleared or sectioned tissues, or to artificial substrates containing mddt. Microarrays are particularly suitable for identifying the presence of and detecting the level of expression for multiple genes of interest by examining gene expression correlated with, e.g., various stages of development, treatment with a drug or compound, or disease progression. An array analogous to a dot or slot blot may be used to arrange and link polynucleotides to the surface of a substrate using one or more of the following: mechanical (vacuum), chemical, thermal, or UV bonding procedures. Such an array may contain any number of mddt and may be produced by hand or by using available devices, materials, and machines.

Microarrays may be prepared, used, and analyzed using methods known in the art. (See, e.g., Brennan, T.M. et al. (1995) U.S. Patent No. 5,474,796; Schena, M. et al. (1996) *Proc. Natl. Acad. Sci. USA* 93:10614-10619; Baldeschweiler et al. (1995) PCT application WO95/251116; Shalon, D. et al. (1995) PCT application WO95/35505; Heller, R.A. et al. (1997) *Proc. Natl. Acad. Sci. USA* 94:2150-2155; and Heller, M.J. et al. (1997) U.S. Patent No. 5,605,662.)

Probes may be labeled by either PCR or enzymatic techniques using a variety of commercially available reporter molecules. For example, commercial kits are available for radioactive and chemiluminescent labeling (Amersham Pharmacia Biotech) and for alkaline phosphatase labeling (Life Technologies). Alternatively, mddt may be cloned into commercially available vectors for the production of RNA probes. Such probes may be transcribed in the presence of at least one labeled nucleotide (e.g., <sup>32</sup>P-ATP, Amersham Pharmacia Biotech).

Additionally the polynucleotides of SEQ ID NO:1-396 or suitable fragments thereof can be

used to isolate full length cDNA sequences utilizing hybridization and/or amplification procedures well known in the art, e.g., cDNA library screening, PCR amplification, etc. The molecular cloning of such full length cDNA sequences may employ the method of cDNA library screening with probes using the hybridization, stringency, washing, and probing strategies described above and in Ausubel, supra,  
5 Chapters 3, 5, and 6. These procedures may also be employed with genomic libraries to isolate genomic sequences of mddt in order to analyze, e.g., regulatory elements.

### Genetic Mapping

Gene identification and mapping are important in the investigation and treatment of almost all  
10 conditions, diseases, and disorders. Cancer, cardiovascular disease, Alzheimer's disease, arthritis, diabetes, and mental illnesses are of particular interest. Each of these conditions is more complex than the single gene defects of sickle cell anemia or cystic fibrosis, with select groups of genes being predictive of predisposition for a particular condition, disease, or disorder. For example, cardiovascular disease may result from malfunctioning receptor molecules that fail to clear cholesterol  
15 from the bloodstream, and diabetes may result when a particular individual's immune system is activated by an infection and attacks the insulin-producing cells of the pancreas. In some studies, Alzheimer's disease has been linked to a gene on chromosome 21; other studies predict a different gene and location. Mapping of disease genes is a complex and reiterative process and generally proceeds from genetic linkage analysis to physical mapping.

20 As a condition is noted among members of a family, a genetic linkage map traces parts of chromosomes that are inherited in the same pattern as the condition. Statistics link the inheritance of particular conditions to particular regions of chromosomes, as defined by RFLP or other markers. (See, for example, Lander, E. S. and Botstein, D. (1986) Proc. Natl. Acad. Sci. USA 83:7353-7357.) Occasionally, genetic markers and their locations are known from previous studies. More often,  
25 however, the markers are simply stretches of DNA that differ among individuals. Examples of genetic linkage maps can be found in various scientific journals or at the Online Mendelian Inheritance in Man (OMIM) World Wide Web site.

In another embodiment of the invention, mddt sequences may be used to generate hybridization probes useful in chromosomal mapping of naturally occurring genomic sequences. Either  
30 coding or noncoding sequences of mddt may be used, and in some instances, noncoding sequences may be preferable over coding sequences. For example, conservation of an mddt coding sequence among members of a multi-gene family may potentially cause undesired cross hybridization during chromosomal mapping. The sequences may be mapped to a particular chromosome, to a specific region of a chromosome, or to artificial chromosome constructions, e.g., human artificial chromosomes  
35 (HACs), yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), bacterial P1

constructions, or single chromosome cDNA libraries. (See, e.g., Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355; Price, C.M. (1993) Blood Rev. 7:127-134; and Trask, B.J. (1991) Trends Genet. 7:149-154.)

Fluorescent in situ hybridization (FISH) may be correlated with other physical chromosome mapping techniques and genetic map data. (See, e.g., Meyers, supra, pp. 965-968.) Correlation between the location of mddt on a physical chromosomal map and a specific disorder, or a predisposition to a specific disorder, may help define the region of DNA associated with that disorder. The mddt sequences may also be used to detect polymorphisms that are genetically linked to the inheritance of a particular condition, disease, or disorder.

In situ hybridization of chromosomal preparations and genetic mapping techniques, such as linkage analysis using established chromosomal markers, may be used for extending existing genetic maps. Often the placement of a gene on the chromosome of another mammalian species, such as mouse, may reveal associated markers even if the number or arm of the corresponding human chromosome is not known. These new marker sequences can be mapped to human chromosomes and may provide valuable information to investigators searching for disease genes using positional cloning or other gene discovery techniques. Once a disease or syndrome has been crudely correlated by genetic linkage with a particular genomic region, e.g., ataxia-telangiectasia to 11q22-23, any sequences mapping to that area may represent associated or regulatory genes for further investigation. (See, e.g., Gatti, R.A. et al. (1988) Nature 336:577-580.) The nucleotide sequences of the subject invention may also be used to detect differences in chromosomal architecture due to translocation, inversion, etc., among normal, carrier, or affected individuals.

Once a disease-associated gene is mapped to a chromosomal region, the gene must be cloned in order to identify mutations or other alterations (e.g., translocations or inversions) that may be correlated with disease. This process requires a physical map of the chromosomal region containing the disease-gene of interest along with associated markers. A physical map is necessary for determining the nucleotide sequence of and order of marker genes on a particular chromosomal region. Physical mapping techniques are well known in the art and require the generation of overlapping sets of cloned DNA fragments from a particular organelle, chromosome, or genome. These clones are analyzed to reconstruct and catalog their order. Once the position of a marker is determined, the DNA from that region is obtained by consulting the catalog and selecting clones from that region. The gene of interest is located through positional cloning techniques using hybridization or similar methods.

#### Diagnostic Uses

The mddt of the present invention may be used to design probes useful in diagnostic assays.

Such assays, well known to those skilled in the art, may be used to detect or confirm conditions, disorders, or diseases associated with abnormal levels of mddt expression. Labeled probes developed from mddt sequences are added to a sample under hybridizing conditions of desired stringency. In some instances, mddt, or fragments or oligonucleotides derived from mddt, may be used as primers in  
5 amplification steps prior to hybridization. The amount of hybridization complex formed is quantified and compared with standards for that cell or tissue. If mddt expression varies significantly from the standard, the assay indicates the presence of the condition, disorder, or disease. Qualitative or quantitative diagnostic methods may include northern, dot blot, or other membrane or dip-stick based technologies or multiple-sample format technologies such as PCR, enzyme-linked immunosorbent  
10 assay (ELISA)-like, pin, or chip-based assays.

The probes described above may also be used to monitor the progress of conditions, disorders, or diseases associated with abnormal levels of mddt expression, or to evaluate the efficacy of a particular therapeutic treatment. The candidate probe may be identified from the mddt that are specific to a given human tissue and have not been observed in GenBank or other genome databases.  
15 Such a probe may be used in animal studies, preclinical tests, clinical trials, or in monitoring the treatment of an individual patient. In a typical process, standard expression is established by methods well known in the art for use as a basis of comparison, samples from patients affected by the disorder or disease are combined with the probe to evaluate any deviation from the standard profile, and a therapeutic agent is administered and effects are monitored to generate a treatment profile. Efficacy  
20 is evaluated by determining whether the expression progresses toward or returns to the standard normal pattern. Treatment profiles may be generated over a period of several days or several months. Statistical methods well known to those skilled in the art may be use to determine the significance of such therapeutic agents.

The polynucleotides are also useful for identifying individuals from minute biological samples,  
25 for example, by matching the RFLP pattern of a sample's DNA to that of an individual's DNA. The polynucleotides of the present invention can also be used to determine the actual base-by-base DNA sequence of selected portions of an individual's genome. These sequences can be used to prepare PCR primers for amplifying and isolating such selected DNA, which can then be sequenced. Using this technique, an individual can be identified through a unique set of DNA sequences. Once a unique  
30 ID database is established for an individual, positive identification of that individual can be made from extremely small tissue samples.

In a particular aspect, oligonucleotide primers derived from the mddt of the invention may be used to detect single nucleotide polymorphisms (SNPs). SNPs are substitutions, insertions and deletions that are a frequent cause of inherited or acquired genetic disease in humans. Methods of  
35 SNP detection include, but are not limited to, single-stranded conformation polymorphism (SSCP) and

fluorescent SSCP (fSSCP) methods. In SSCP, oligonucleotide primers derived from mddt are used to amplify DNA using the polymerase chain reaction (PCR). The DNA may be derived, for example, from diseased or normal tissue, biopsy samples, bodily fluids, and the like. SNPs in the DNA cause differences in the secondary and tertiary structures of PCR products in single-stranded form, and these differences are detectable using gel electrophoresis in non-denaturing gels. In fSSCP, the oligonucleotide primers are fluorescently labeled, which allows detection of the amplimers in high-throughput equipment such as DNA sequencing machines. Additionally, sequence database analysis methods, termed in silico SNP (isSNP), are capable of identifying polymorphisms by comparing the sequences of individual overlapping DNA fragments which assemble into a common consensus sequence. These computer-based methods filter out sequence variations due to laboratory preparation of DNA and sequencing errors using statistical models and automated analyses of DNA sequence chromatograms. In the alternative, SNPs may be detected and characterized by mass spectrometry using, for example, the high throughput MASSARRAY system (Sequenom, Inc., San Diego CA).

DNA-based identification techniques are critical in forensic technology. DNA sequences taken from very small biological samples such as tissues, e.g., hair or skin, or body fluids, e.g., blood, saliva, semen, etc., can be amplified using, e.g., PCR, to identify individuals. (See, e.g., Erlich, H. (1992) PCR Technology, Freeman and Co., New York, NY). Similarly, polynucleotides of the present invention can be used as polymorphic markers.

There is also a need for reagents capable of identifying the source of a particular tissue. Appropriate reagents can comprise, for example, DNA probes or primers prepared from the sequences of the present invention that are specific for particular tissues. Panels of such reagents can identify tissue by species and/or by organ type. In a similar fashion, these reagents can be used to screen tissue cultures for contamination.

The polynucleotides of the present invention can also be used as molecular weight markers on nucleic acid gels or Southern blots, as diagnostic probes for the presence of a specific mRNA in a particular cell type, in the creation of subtracted cDNA libraries which aid in the discovery of novel polynucleotides, in selection and synthesis of oligomers for attachment to an array or other support, and as an antigen to elicit an immune response.

#### Disease Model Systems Using mddt

The mddt of the invention or their mammalian homologs may be "knocked out" in an animal model system using homologous recombination in embryonic stem (ES) cells. Such techniques are well known in the art and are useful for the generation of animal models of human disease. (See, e.g., U.S. Patent Number 5,175,383 and U.S. Patent Number 5,767,337.) For example, mouse ES cells, such as the mouse 129/SvJ cell line, are derived from the early mouse embryo and grown in culture. The ES cells are transformed with a vector containing the gene of interest disrupted by a marker gene,

e.g., the neomycin phosphotransferase gene (neo; Capecchi, M.R. (1989) Science 244:1288-1292).

The vector integrates into the corresponding region of the host genome by homologous recombination. Alternatively, homologous recombination takes place using the Cre-loxP system to knockout a gene of interest in a tissue- or developmental stage-specific manner (Marth, J.D. (1996) Clin. Invest. 97:1999-2002; Wagner, K.U. et al. (1997) Nucleic Acids Res. 25:4323-4330). Transformed ES cells are identified and microinjected into mouse cell blastocysts such as those from the C57BL/6 mouse strain. The blastocysts are surgically transferred to pseudopregnant dams, and the resulting chimeric progeny are genotyped and bred to produce heterozygous or homozygous strains. Transgenic animals thus generated may be tested with potential therapeutic or toxic agents.

10       The mddt of the invention may also be manipulated in vitro in ES cells derived from human blastocysts. Human ES cells have the potential to differentiate into at least eight separate cell lineages including endoderm, mesoderm, and ectodermal cell types. These cell lineages differentiate into, for example, neural cells, hematopoietic lineages, and cardiomyocytes (Thomson, J.A. et al. (1998) Science 282:1145-1147).

15       The mddt of the invention can also be used to create “knockin” humanized animals (pigs) or transgenic animals (mice or rats) to model human disease. With knockin technology, a region of mddt is injected into animal ES cells, and the injected sequence integrates into the animal cell genome. Transformed cells are injected into blastulae, and the blastulae are implanted as described above. Transgenic progeny or inbred lines are studied and treated with potential pharmaceutical agents to obtain information on treatment of a human disease. Alternatively, a mammal inbred to overexpress mddt, resulting, e.g., in the secretion of MDDT in its milk, may also serve as a convenient source of that protein (Janne, J. et al. (1998) Biotechnol. Annu. Rev. 4:55-74).

### Screening Assays

25       MDDT encoded by polynucleotides of the present invention may be used to screen for molecules that bind to or are bound by the encoded polypeptides. The binding of the polypeptide and the molecule may activate (agonist), increase, inhibit (antagonist), or decrease activity of the polypeptide or the bound molecule. Examples of such molecules include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

30       Preferably, the molecule is closely related to the natural ligand of the polypeptide, e.g., a ligand or fragment thereof, a natural substrate, or a structural or functional mimetic. (See, Coligan et al., (1991) Current Protocols in Immunology 1(2): Chapter 5.) Similarly, the molecule can be closely related to the natural receptor to which the polypeptide binds, or to at least a fragment of the receptor, e.g., the active site. In either case, the molecule can be rationally designed using known techniques.

35       Preferably, the screening for these molecules involves producing appropriate cells which express the



polypeptide, either as a secreted protein or on the cell membrane. Preferred cells include cells from mammals, yeast, Drosophila, or E. coli. Cells expressing the polypeptide or cell membrane fractions which contain the expressed polypeptide are then contacted with a test compound and binding, stimulation, or inhibition of activity of either the polypeptide or the molecule is analyzed.

5       An assay may simply test binding of a candidate compound to the polypeptide, wherein binding is detected by a fluorophore, radioisotope, enzyme conjugate, or other detectable label. Alternatively, the assay may assess binding in the presence of a labeled competitor.

      Additionally, the assay can be carried out using cell-free preparations, polypeptide/molecule affixed to a solid support, chemical libraries, or natural product mixtures. The assay may also simply  
10   comprise the steps of mixing a candidate compound with a solution containing a polypeptide, measuring polypeptide/molecule activity or binding, and comparing the polypeptide/molecule activity or binding to a standard.

      Preferably, an ELISA assay using, e.g., a monoclonal or polyclonal antibody, can measure polypeptide level in a sample. The antibody can measure polypeptide level by either binding, directly  
15   or indirectly, to the polypeptide or by competing with the polypeptide for a substrate.

      All of the above assays can be used in a diagnostic or prognostic context. The molecules discovered using these assays can be used to treat disease or to bring about a particular result in a patient (e.g., blood vessel growth) by activating or inhibiting the polypeptide/molecule. Moreover, the assays can discover agents which may inhibit or enhance the production of the polypeptide from  
20   suitably manipulated cells or tissues.

### Transcript Imaging and Toxicological Testing

      Another embodiment relates to the use of mddt to develop a transcript image of a tissue or cell type. A transcript image represents the global pattern of gene expression by a particular tissue or  
25   cell type. Global gene expression patterns are analyzed by quantifying the number of expressed genes and their relative abundance under given conditions and at a given time. (See Seilhamer et al., "Comparative Gene Transcript Analysis," U.S. Patent Number 5,840,484, expressly incorporated by reference herein.) Thus a transcript image may be generated by hybridizing the polynucleotides of the present invention or their complements to the totality of transcripts or reverse transcripts of a  
30   particular tissue or cell type. In one embodiment, the hybridization takes place in high-throughput format, wherein the polynucleotides of the present invention or their complements comprise a subset of a plurality of elements on a microarray. The resultant transcript image would provide a profile of gene activity pertaining to disease detection and treatment molecules.

      Transcript images which profile mddt expression may be generated using transcripts isolated  
35   from tissues, cell lines, biopsies, or other biological samples. The transcript image may thus reflect

mddt expression in vivo, as in the case of a tissue or biopsy sample, or in vitro, as in the case of a cell line.

Transcript images which profile mddt expression may also be used in conjunction with in vitro model systems and preclinical evaluation of pharmaceuticals, as well as toxicological testing of industrial and naturally-occurring environmental compounds. All compounds induce characteristic gene expression patterns, frequently termed molecular fingerprints or toxicant signatures, which are indicative of mechanisms of action and toxicity (Nuwaysir, E. F. et al. (1999) Mol. Carcinog. 24:153-159; Steiner, S. and Anderson, N. L. (2000) Toxicol. Lett. 112-113:467-71, expressly incorporated by reference herein). If a test compound has a signature similar to that of a compound with known toxicity, it is likely to share those toxic properties. These fingerprints or signatures are most useful and refined when they contain expression information from a large number of genes and gene families. Ideally, a genome-wide measurement of expression provides the highest quality signature. Even genes whose expression is not altered by any tested compounds are important as well, as the levels of expression of these genes are used to normalize the rest of the expression data. The normalization procedure is useful for comparison of expression data after treatment with different compounds. While the assignment of gene function to elements of a toxicant signature aids in interpretation of toxicity mechanisms, knowledge of gene function is not necessary for the statistical matching of signatures which leads to prediction of toxicity. (See, for example, Press Release 00-02 from the National Institute of Environmental Health Sciences, released February 29, 2000, available at <http://www.niehs.nih.gov/oc/news/toxchip.htm>.) Therefore, it is important and desirable in toxicological screening using toxicant signatures to include all expressed gene sequences.

In one embodiment, the toxicity of a test compound is assessed by treating a biological sample containing nucleic acids with the test compound. Nucleic acids that are expressed in the treated biological sample are hybridized with one or more probes specific to the polynucleotides of the present invention, so that transcript levels corresponding to the polynucleotides of the present invention may be quantified. The transcript levels in the treated biological sample are compared with levels in an untreated biological sample. Differences in the transcript levels between the two samples are indicative of a toxic response caused by the test compound in the treated sample.

Another particular embodiment relates to the use of MDDT encoded by polynucleotides of the present invention to analyze the proteome of a tissue or cell type. The term proteome refers to the global pattern of protein expression in a particular tissue or cell type. Each protein component of a proteome can be subjected individually to further analysis. Proteome expression patterns, or profiles, are analyzed by quantifying the number of expressed proteins and their relative abundance under given conditions and at a given time. A profile of a cell's proteome may thus be generated by separating and analyzing the polypeptides of a particular tissue or cell type. In one embodiment, the

separation is achieved using two-dimensional gel electrophoresis, in which proteins from a sample are separated by isoelectric focusing in the first dimension, and then according to molecular weight by sodium dodecyl sulfate slab gel electrophoresis in the second dimension (Steiner and Anderson, supra). The proteins are visualized in the gel as discrete and uniquely positioned spots, typically by staining the gel with an agent such as Coomassie Blue or silver or fluorescent stains. The optical density of each protein spot is generally proportional to the level of the protein in the sample. The optical densities of equivalently positioned protein spots from different samples, for example, from biological samples either treated or untreated with a test compound or therapeutic agent, are compared to identify any changes in protein spot density related to the treatment. The proteins in the spots are partially sequenced using, for example, standard methods employing chemical or enzymatic cleavage followed by mass spectrometry. The identity of the protein in a spot may be determined by comparing its partial sequence, preferably of at least 5 contiguous amino acid residues, to the polypeptide sequences of the present invention. In some cases, further sequence data may be obtained for definitive protein identification.

A proteomic profile may also be generated using antibodies specific for MDDT to quantify the levels of MDDT expression. In one embodiment, the antibodies are used as elements on a microarray, and protein expression levels are quantified by exposing the microarray to the sample and detecting the levels of protein bound to each array element (Lueking, A. et al. (1999) *Anal. Biochem.* 270:103-11; Mendoz, L. G. et al. (1999) *Biotechniques* 27:778-88). Detection may be performed by a variety of methods known in the art, for example, by reacting the proteins in the sample with a thiol- or amino-reactive fluorescent compound and detecting the amount of fluorescence bound at each array element.

Toxicant signatures at the proteome level are also useful for toxicological screening, and should be analyzed in parallel with toxicant signatures at the transcript level. There is a poor correlation between transcript and protein abundances for some proteins in some tissues (Anderson, N. L. and Seilhamer, J. (1997) *Electrophoresis* 18:533-537), so proteome toxicant signatures may be useful in the analysis of compounds which do not significantly affect the transcript image, but which alter the proteomic profile. In addition, the analysis of transcripts in body fluids is difficult, due to rapid degradation of mRNA, so proteomic profiling may be more reliable and informative in such cases.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins that are expressed in the treated biological sample are separated so that the amount of each protein can be quantified. The amount of each protein is compared to the amount of the corresponding protein in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample. Individual proteins are identified by sequencing the amino acid

residues of the individual proteins and comparing these partial sequences to the MDDT encoded by polynucleotides of the present invention.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins from the biological sample are incubated with antibodies specific to the MDDT encoded by polynucleotides of the present invention. The amount of protein recognized by the antibodies is quantified. The amount of protein in the treated biological sample is compared with the amount in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample.

Transcript images may be used to profile mddt expression in distinct tissue types. This process can be used to determine disease detection and treatment molecule activity in a particular tissue type relative to this activity in a different tissue type. Transcript images may be used to generate a profile of mddt expression characteristic of diseased tissue. Transcript images of tissues before and after treatment may be used for diagnostic purposes, to monitor the progression of disease, and to monitor the efficacy of drug treatments for diseases which affect the activity of disease detection and treatment molecules.

Transcript images of cell lines can be used to assess disease detection and treatment molecule activity and/or to identify cell lines that lack or misregulate this activity. Such cell lines may then be treated with pharmaceutical agents, and a transcript image following treatment may indicate the efficacy of these agents in restoring desired levels of this activity. A similar approach may be used to assess the toxicity of pharmaceutical agents as reflected by undesirable changes in disease detection and treatment molecule activity. Candidate pharmaceutical agents may be evaluated by comparing their associated transcript images with those of pharmaceutical agents of known effectiveness.

#### Antisense Molecules

The polynucleotides of the present invention are useful in antisense technology. Antisense technology or therapy relies on the modulation of expression of a target protein through the specific binding of an antisense sequence to a target sequence encoding the target protein or directing its expression. (See, e.g., Agrawal, S., ed. (1996) Antisense Therapeutics, Humana Press Inc., Totawa NJ; Alama, A. et al. (1997) *Pharmacol. Res.* 36(3):171-178; Crooke, S.T. (1997) *Adv. Pharmacol.* 40:1-49; Sharma, H.W. and R. Narayanan (1995) *Bioessays* 17(12):1055-1063; and Lavrosky, Y. et al. (1997) *Biochem. Mol. Med.* 62(1):11-22.) An antisense sequence is a polynucleotide sequence capable of specifically hybridizing to at least a portion of the target sequence. Antisense sequences bind to cellular mRNA and/or genomic DNA, affecting translation and/or transcription. Antisense sequences can be DNA, RNA, or nucleic acid mimics and analogs. (See, e.g., Rossi, J.J. et al. (1991)

Antisense Res. Dev. 1(3):285-288; Lee, R. et al. (1998) Biochemistry 37(3):900-1010; Pardridge, W.M. et al. (1995) Proc. Natl. Acad. Sci. USA 92(12):5592-5596; and Nielsen, P. E. and Haaima, G. (1997) Chem. Soc. Rev. 96:73-78.) Typically, the binding which results in modulation of expression occurs through hybridization or binding of complementary base pairs. Antisense sequences can also  
5 bind to DNA duplexes through specific interactions in the major groove of the double helix.

The polynucleotides of the present invention and fragments thereof can be used as antisense sequences to modify the expression of the polypeptide encoded by mddt. The antisense sequences can be produced ex vivo, such as by using any of the ABI nucleic acid synthesizer series (Applied Biosystems) or other automated systems known in the art. Antisense sequences can also be produced  
10 biologically, such as by transforming an appropriate host cell with an expression vector containing the sequence of interest. (See, e.g., Agrawal, supra.)

In therapeutic use, any gene delivery system suitable for introduction of the antisense sequences into appropriate target cells can be used. Antisense sequences can be delivered intracellularly in the form of an expression plasmid which, upon transcription, produces a sequence  
15 complementary to at least a portion of the cellular sequence encoding the target protein. (See, e.g., Slater, J.E., et al. (1998) J. Allergy Clin. Immunol. 102(3):469-475; and Scanlon, K.J., et al. (1995) 9(13):1288-1296.) Antisense sequences can also be introduced intracellularly through the use of viral vectors, such as retrovirus and adeno-associated virus vectors. (See, e.g., Miller, A.D. (1990) Blood 76:271; Ausubel, F.M. et al. (1995) Current Protocols in Molecular Biology, John Wiley & Sons, New  
20 York NY; Uckert, W. and W. Walther (1994) Pharmacol. Ther. 63(3):323-347.) Other gene delivery mechanisms include liposome-derived systems, artificial viral envelopes, and other systems known in the art. (See, e.g., Rossi, J.J. (1995) Br. Med. Bull. 51(1):217-225; Boado, R.J. et al. (1998) J. Pharm. Sci. 87(11):1308-1315; and Morris, M.C. et al. (1997) Nucleic Acids Res. 25(14):2730-2736.)

## 25 Expression

In order to express a biologically active MDDT, the nucleotide sequences encoding MDDT or fragments thereof may be inserted into an appropriate expression vector, i.e., a vector which contains the necessary elements for transcriptional and translational control of the inserted coding sequence in a suitable host. Methods which are well known to those skilled in the art may be used to construct  
30 expression vectors containing sequences encoding MDDT and appropriate transcriptional and translational control elements. These methods include in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. (See, e.g., Sambrook, supra, Chapters 4, 8, 16, and 17; and Ausubel, supra, Chapters 9, 10, 13, and 16.)

A variety of expression vector/host systems may be utilized to contain and express sequences  
35 encoding MDDT. These include, but are not limited to, microorganisms such as bacteria transformed

with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with viral expression vectors (e.g., baculovirus); plant cell systems transformed with viral expression vectors (e.g., cauliflower mosaic virus, CaMV, or tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or  
 5 animal (mammalian) cell systems. (See, e.g., Sambrook, supra; Ausubel, 1995, supra, Van Heeke, G. and S.M. Schuster (1989) J. Biol. Chem. 264:5503-5509; Bitter, G.A. et al. (1987) Methods Enzymol. 153:516-544; Scorer, C.A. et al. (1994) Bio/Technology 12:181-184; Engelhard, E.K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945; Takamatsu, N. (1987) EMBO J. 6:307-311; Coruzzi, G. et al. (1984) EMBO J. 3:1671-1680; Broglie,  
 10 R. et al. (1984) Science 224:838-843; Winter, J. et al. (1991) Results Probl. Cell Differ. 17:85-105; The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp. 191-196; Logan, J. and T. Shenk (1984) Proc. Natl. Acad. Sci. USA 81:3655-3659; and Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355.) Expression vectors derived from retroviruses, adenoviruses, or herpes or vaccinia viruses, or from various bacterial plasmids, may be used for  
 15 delivery of nucleotide sequences to the targeted organ, tissue, or cell population. (See, e.g., Di Nicola, M. et al. (1998) Cancer Gen. Ther. 5(6):350-356; Yu, M. et al., (1993) Proc. Natl. Acad. Sci. USA 90(13):6340-6344; Buller, R.M. et al. (1985) Nature 317(6040):813-815; McGregor, D.P. et al. (1994) Mol. Immunol. 31(3):219-226; and Verma, I.M. and N. Somia (1997) Nature 389:239-242.) The invention is not limited by the host cell employed.

20 For long term production of recombinant proteins in mammalian systems, stable expression of MDDT in cell lines is preferred. For example, sequences encoding MDDT can be transformed into cell lines using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Any number of selection systems may be used to recover transformed cell lines. (See, e.g., Wigler, M. et al.  
 25 (1977) Cell 11:223-232; Lowy, I. et al. (1980) Cell 22:817-823.; Wigler, M. et al. (1980) Proc. Natl. Acad. Sci. USA 77:3567-3570; Colbere-Garapin, F. et al. (1981) J. Mol. Biol. 150:1-14; Hartman, S.C. and R.C. Mulligan (1988) Proc. Natl. Acad. Sci. USA 85:8047-8051; Rhodes, C.A. (1995) Methods Mol. Biol. 55:121-131.)

### 30 Therapeutic Uses of mddt

The mddt of the invention may be used for somatic or germline gene therapy. Gene therapy may be performed to (i) correct a genetic deficiency (e.g., in the cases of severe combined immunodeficiency (SCID)-X1 disease characterized by X-linked inheritance (Cavazzana-Calvo, M. et al. (2000) Science 288:669-672), severe combined immunodeficiency syndrome associated with an  
 35 inherited adenosine deaminase (ADA) deficiency (Blaese, R.M. et al. (1995) Science 270:475-480;

Bordignon, C. et al. (1995) *Science* 270:470-475), cystic fibrosis (Zabner, J. et al. (1993) *Cell* 75:207-216; Crystal, R.G. et al. (1995) *Hum. Gene Therapy* 6:643-666; Crystal, R.G. et al. (1995) *Hum. Gene Therapy* 6:667-703), thalassemias, familial hypercholesterolemia, and hemophilia resulting from Factor VIII or Factor IX deficiencies (Crystal, R.G. (1995) *Science* 270:404-410; Verma, I.M. and Somia, N. (1997) *Nature* 389:239-242)), (ii) express a conditionally lethal gene product (e.g., in the case of cancers which result from unregulated cell proliferation), or (iii) express a protein which affords protection against intracellular parasites (e.g., against human retroviruses, such as human immunodeficiency virus (HIV) (Baltimore, D. (1988) *Nature* 335:395-396; Poeschla, E. et al. (1996) *Proc. Natl. Acad. Sci. USA.* 93:11395-11399), hepatitis B or C virus (HBV, HCV); fungal parasites, such as Candida albicans and Paracoccidioides brasiliensis; and protozoan parasites such as Plasmodium falciparum and Trypanosoma cruzi). In the case where a genetic deficiency in mddt expression or regulation causes disease, the expression of mddt from an appropriate population of transduced cells may alleviate the clinical manifestations caused by the genetic deficiency.

In a further embodiment of the invention, diseases or disorders caused by deficiencies in mddt are treated by constructing mammalian expression vectors comprising mddt and introducing these vectors by mechanical means into mddt-deficient cells. Mechanical transfer technologies for use with cells in vivo or ex vitro include (i) direct DNA microinjection into individual cells, (ii) ballistic gold particle delivery, (iii) liposome-mediated transfection, (iv) receptor-mediated gene transfer, and (v) the use of DNA transposons (Morgan, R.A. and Anderson, W.F. (1993) *Annu. Rev. Biochem.* 62:191-217; Ivics, Z. (1997) *Cell* 91:501-510; Boulay, J-L. and Récipon, H. (1998) *Curr. Opin. Biotechnol.* 9:445-450).

Expression vectors that may be effective for the expression of mddt include, but are not limited to, the PCDNA 3.1, EPITAG, PRCCMV2, PREP, PVAX vectors (Invitrogen, Carlsbad CA), PCMV-SCRIPT, PCMV-TAG, PEGSH/PERV (Stratagene, La Jolla CA), and PTET-OFF, PTET-ON, PTRE2, PTRE2-LUC, PTK-HYG (Clontech, Palo Alto CA). The mddt of the invention may be expressed using (i) a constitutively active promoter, (e.g., from cytomegalovirus (CMV), Rous sarcoma virus (RSV), SV40 virus, thymidine kinase (TK), or  $\beta$ -actin genes), (ii) an inducible promoter (e.g., the tetracycline-regulated promoter (Gossen, M. and Bujard, H. (1992) *Proc. Natl. Acad. Sci. U.S.A.* 89:5547-5551; Gossen, M. et al., (1995) *Science* 268:1766-1769; Rossi, F.M.V. and Blau, H.M. (1998) *Curr. Opin. Biotechnol.* 9:451-456), commercially available in the T-REX plasmid (Invitrogen); the ecdysone-inducible promoter (available in the plasmids PVGRXR and PIND; Invitrogen); the FK506/rapamycin inducible promoter; or the RU486/mifepristone inducible promoter (Rossi, F.M.V. and Blau, H.M. supra), or (iii) a tissue-specific promoter or the native promoter of the endogenous gene encoding MDDT from a normal individual.

Commercially available liposome transformation kits (e.g., the PERFECT LIPID TRANSFECTION KIT, available from Invitrogen) allow one with ordinary skill in the art to deliver polynucleotides to target cells in culture and require minimal effort to optimize experimental parameters. In the alternative, transformation is performed using the calcium phosphate method (Graham, F.L. and Eb, A.J. (1973) *Virology* 52:456-467), or by electroporation (Neumann, E. et al. (1982) *EMBO J.* 1:841-845). The introduction of DNA to primary cells requires modification of these standardized mammalian transfection protocols.

In another embodiment of the invention, diseases or disorders caused by genetic defects with respect to mddt expression are treated by constructing a retrovirus vector consisting of (i) mddt under the control of an independent promoter or the retrovirus long terminal repeat (LTR) promoter, (ii) appropriate RNA packaging signals, and (iii) a Rev-responsive element (RRE) along with additional retrovirus *cis*-acting RNA sequences and coding sequences required for efficient vector propagation. Retrovirus vectors (e.g., PFB and PFBNEO) are commercially available (Stratagene) and are based on published data (Riviere, I. et al. (1995) *Proc. Natl. Acad. Sci. U.S.A.* 92:6733-6737), incorporated by reference herein. The vector is propagated in an appropriate vector producing cell line (VPCL) that expresses an envelope gene with a tropism for receptors on the target cells or a promiscuous envelope protein such as VSVg (Armentano, D. et al. (1987) *J. Virol.* 61:1647-1650; Bender, M.A. et al. (1987) *J. Virol.* 61:1639-1646; Adam, M.A. and Miller, A.D. (1988) *J. Virol.* 62:3802-3806; Dull, T. et al. (1998) *J. Virol.* 72:8463-8471; Zufferey, R. et al. (1998) *J. Virol.* 72:9873-9880). U.S. Patent Number 5,910,434 to Rigg ("Method for obtaining retrovirus packaging cell lines producing high transducing efficiency retroviral supernatant") discloses a method for obtaining retrovirus packaging cell lines and is hereby incorporated by reference. Propagation of retrovirus vectors, transduction of a population of cells (e.g., CD4<sup>+</sup> T-cells), and the return of transduced cells to a patient are procedures well known to persons skilled in the art of gene therapy and have been well documented (Ranga, U. et al. (1997) *J. Virol.* 71:7020-7029; Bauer, G. et al. (1997) *Blood* 89:2259-2267; Bonyhadi, M.L. (1997) *J. Virol.* 71:4707-4716; Ranga, U. et al. (1998) *Proc. Natl. Acad. Sci. U.S.A.* 95:1201-1206; Su, L. (1997) *Blood* 89:2283-2290).

In the alternative, an adenovirus-based gene therapy delivery system is used to deliver mddt to cells which have one or more genetic abnormalities with respect to the expression of mddt. The construction and packaging of adenovirus-based vectors are well known to those with ordinary skill in the art. Replication defective adenovirus vectors have proven to be versatile for importing genes encoding immunoregulatory proteins into intact islets in the pancreas (Csete, M.E. et al. (1995) *Transplantation* 27:263-268). Potentially useful adenoviral vectors are described in U.S. Patent Number 5,707,618 to Armentano ("Adenovirus vectors for gene therapy"), hereby incorporated by



reference. For adenoviral vectors, see also Antinuzzi, P.A. et al. (1999) *Annu. Rev. Nutr.* 19:511-544 and Verma, I.M. and Somia, N. (1997) *Nature* 18:389:239-242, both incorporated by reference herein.

In another alternative, a herpes-based, gene therapy delivery system is used to deliver mddt to target cells which have one or more genetic abnormalities with respect to the expression of mddt. The use of herpes simplex virus (HSV)-based vectors may be especially valuable for introducing mddt to cells of the central nervous system, for which HSV has a tropism. The construction and packaging of herpes-based vectors are well known to those with ordinary skill in the art. A replication-competent herpes simplex virus (HSV) type 1-based vector has been used to deliver a reporter gene to the eyes of primates (Liu, X. et al. (1999) *Exp. Eye Res.* 169:385-395). The construction of a HSV-1 virus vector has also been disclosed in detail in U.S. Patent Number 5,804,413 to DeLuca ("Herpes simplex virus strains for gene transfer"), which is hereby incorporated by reference. U.S. Patent Number 5,804,413 teaches the use of recombinant HSV d92 which consists of a genome containing at least one exogenous gene to be transferred to a cell under the control of the appropriate promoter for purposes including human gene therapy. Also taught by this patent are the construction and use of recombinant HSV strains deleted for ICP4, ICP27 and ICP22. For HSV vectors, see also Goins, W. F. et al. 1999 *J. Virol.* 73:519-532 and Xu, H. et al., (1994) *Dev. Biol.* 163:152-161, hereby incorporated by reference. The manipulation of cloned herpesvirus sequences, the generation of recombinant virus following the transfection of multiple plasmids containing different segments of the large herpesvirus genomes, the growth and propagation of herpesvirus, and the infection of cells with herpesvirus are techniques well known to those of ordinary skill in the art.

In another alternative, an alphavirus (positive, single-stranded RNA virus) vector is used to deliver mddt to target cells. The biology of the prototypic alphavirus, Semliki Forest Virus (SFV), has been studied extensively and gene transfer vectors have been based on the SFV genome (Garoff, H. and Li, K-J. (1998) *Curr. Opin. Biotech.* 9:464-469). During alphavirus RNA replication, a subgenomic RNA is generated that normally encodes the viral capsid proteins. This subgenomic RNA replicates to higher levels than the full-length genomic RNA, resulting in the overproduction of capsid proteins relative to the viral proteins with enzymatic activity (e.g., protease and polymerase). Similarly, inserting mddt into the alphavirus genome in place of the capsid-coding region results in the production of a large number of mddt RNAs and the synthesis of high levels of MDDT in vector transduced cells. While alphavirus infection is typically associated with cell lysis within a few days, the ability to establish a persistent infection in hamster normal kidney cells (BHK-21) with a variant of Sindbis virus (SIN) indicates that the lytic replication of alphaviruses can be altered to suit the needs of the gene therapy application (Dryga, S.A. et al. (1997) *Virology* 228:74-83). The wide host range of alphaviruses will allow the introduction of mddt into a variety of cell types. The specific transduction of a subset of cells in a population may require the sorting of cells prior to transduction. The methods

of manipulating infectious cDNA clones of alphaviruses, performing alphavirus cDNA and RNA transfections, and performing alphavirus infections, are well known to those with ordinary skill in the art.

5    Antibodies

Anti-MDDT antibodies may be used to analyze protein expression levels. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, and Fab fragments. For descriptions of and protocols of antibody technologies, see, e.g., Pound J.D. (1998) Immunochemical Protocols, Humana Press, Totowa, NJ.

10       The amino acid sequence encoded by the mddt of the Sequence Listing may be analyzed by appropriate software (e.g., LASERGENE NAVIGATOR software, DNASTAR) to determine regions of high immunogenicity. The optimal sequences for immunization are selected from the C-terminus, the N-terminus, and those intervening, hydrophilic regions of the polypeptide which are likely to be exposed to the external environment when the polypeptide is in its natural conformation.

15       Analysis used to select appropriate epitopes is also described by Ausubel (1997, supra, Chapter 11.7). Peptides used for antibody induction do not need to have biological activity; however, they must be antigenic. Peptides used to induce specific antibodies may have an amino acid sequence consisting of at least five amino acids, preferably at least 10 amino acids, and most preferably at least 15 amino acids. A peptide which mimics an antigenic fragment of the natural polypeptide may be fused with  
20       another protein such as keyhole hemolimpet cyanin (KLH; Sigma, St. Louis MO) for antibody production. A peptide encompassing an antigenic region may be expressed from an mddt, synthesized as described above, or purified from human cells.

Procedures well known in the art may be used for the production of antibodies. Various hosts including mice, goats, and rabbits, may be immunized by injection with a peptide. Depending on the  
25       host species, various adjuvants may be used to increase immunological response.

In one procedure, peptides about 15 residues in length may be synthesized using an ABI 431A peptide synthesizer (Applied Biosystems) using fmoc-chemistry and coupled to KLH (Sigma) by reaction with M-maleimidobenzoyl-N-hydroxysuccinimide ester (Ausubel, 1995, supra). Rabbits are immunized with the peptide-KLH complex in complete Freund's adjuvant. The resulting antisera are  
30       tested for anti-peptide activity by binding the peptide to plastic, blocking with 1% bovine serum albumin (BSA), reacting with rabbit antisera, washing, and reacting with radioiodinated goat anti-rabbit IgG. Antisera with anti-peptide activity are tested for anti-MDDT activity using protocols well known in the art, including ELISA, radioimmunoassay (RIA), and immunoblotting.

In another procedure, isolated and purified peptide may be used to immunize mice (about 100  
35       μg of peptide) or rabbits (about 1 mg of peptide). Subsequently, the peptide is radioiodinated and used

to screen the immunized animals' B-lymphocytes for production of antipeptide antibodies. Positive cells are then used to produce hybridomas using standard techniques. About 20 mg of peptide is sufficient for labeling and screening several thousand clones. Hybridomas of interest are detected by screening with radioiodinated peptide to identify those fusions producing peptide-specific monoclonal antibody. In a typical protocol, wells of a multi-well plate (FAST, Becton-Dickinson, Palo Alto, CA) are coated with affinity-purified, specific rabbit-anti-mouse (or suitable anti-species IgG) antibodies at 10 mg/ml. The coated wells are blocked with 1% BSA and washed and exposed to supernatants from hybridomas. After incubation, the wells are exposed to radiolabeled peptide at 1 mg/ml.

Clones producing antibodies bind a quantity of labeled peptide that is detectable above background. Such clones are expanded and subjected to 2 cycles of cloning. Cloned hybridomas are injected into pristane-treated mice to produce ascites, and monoclonal antibody is purified from the ascitic fluid by affinity chromatography on protein A (Amersham Pharmacia Biotech). Several procedures for the production of monoclonal antibodies, including *in vitro* production, are described in Pound (*supra*). Monoclonal antibodies with antipeptide activity are tested for anti-MDDT activity using protocols well known in the art, including ELISA, RIA, and immunoblotting.

Antibody fragments containing specific binding sites for an epitope may also be generated. For example, such fragments include, but are not limited to, the F(ab')<sub>2</sub> fragments produced by pepsin digestion of the antibody molecule, and the Fab fragments generated by reducing the disulfide bridges of the F(ab')<sub>2</sub> fragments. Alternatively, construction of Fab expression libraries in filamentous bacteriophage allows rapid and easy identification of monoclonal fragments with desired specificity (Pound, *supra*, Chaps. 45-47). Antibodies generated against polypeptide encoded by mddt can be used to purify and characterize full-length MDDT protein and its activity, binding partners, etc.

#### Assays Using Antibodies

Anti-MDDT antibodies may be used in assays to quantify the amount of MDDT found in a particular human cell. Such assays include methods utilizing the antibody and a label to detect expression level under normal or disease conditions. The peptides and antibodies of the invention may be used with or without modification or labeled by joining them, either covalently or noncovalently, with a reporter molecule.

Protocols for detecting and measuring protein expression using either polyclonal or monoclonal antibodies are well known in the art. Examples include ELISA, RIA, and fluorescent activated cell sorting (FACS). Such immunoassays typically involve the formation of complexes between the MDDT and its specific antibody and the measurement of such complexes. These and other assays are described in Pound (*supra*).

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following preferred specific embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

5 The disclosures of all patents, applications, and publications mentioned above and below, including U.S. Ser. No. 60/280,067, U.S. Ser. No. 60/279,619, U.S. Ser. No. 60/280,068, U.S. Ser. No. 60/291,280, U.S. Ser. No. 60/291,849, U.S. Ser. No. 60/291,829, U.S. Ser. No. 60/299,428, U.S. Ser. No. 60/300,001, and U.S. Ser. No. 60/299,776, are hereby expressly incorporated by reference.

## 10 EXAMPLES

### I. Construction of cDNA Libraries

RNA was purchased from CLONTECH Laboratories, Inc. (Palo Alto CA) or isolated from various tissues. Some tissues were homogenized and lysed in guanidinium isothiocyanate, while others were homogenized and lysed in phenol or in a suitable mixture of denaturants, such as TRIZOL (Life  
15 Technologies), a monophasic solution of phenol and guanidine isothiocyanate. The resulting lysates were centrifuged over CsCl cushions or extracted with chloroform. RNA was precipitated with either isopropanol or sodium acetate and ethanol, or by other routine methods.

Phenol extraction and precipitation of RNA were repeated as necessary to increase RNA purity. In most cases, RNA was treated with DNase. For most libraries, poly(A+) RNA was isolated  
20 using oligo d(T)-coupled paramagnetic particles (Promega Corporation (Promega), Madison WI), OLIGOTEX latex particles (QIAGEN, Inc. (QIAGEN), Valencia CA), or an OLIGOTEX mRNA purification kit (QIAGEN). Alternatively, RNA was isolated directly from tissue lysates using other RNA isolation kits, e.g., the POLY(A)PURE mRNA purification kit (Ambion, Inc., Austin TX).

In some cases, Stratagene was provided with RNA and constructed the corresponding cDNA  
25 libraries. Otherwise, cDNA was synthesized and cDNA libraries were constructed with the UNIZAP vector system (Stratagene Cloning Systems, Inc. (Stratagene), La Jolla CA) or SUPERScript plasmid system (Life Technologies), using the recommended procedures or similar methods known in the art. (See, e.g., Ausubel, 1997, supra, Chapters 5.1 through 6.6.) Reverse transcription was initiated using oligo d(T) or random primers. Synthetic oligonucleotide adapters  
30 were ligated to double stranded cDNA, and the cDNA was digested with the appropriate restriction enzyme or enzymes. For most libraries, the cDNA was size-selected (300-1000 bp) using SEPHACRYL S1000, SEPHAROSE CL2B, or SEPHAROSE CL4B column chromatography (Amersham Pharmacia Biotech) or preparative agarose gel electrophoresis. cDNAs were ligated into compatible restriction enzyme sites of the polylinker of a suitable plasmid, e.g., PBLUESCRIPT  
35 plasmid (Stratagene), PSPOrt1 plasmid (Life Technologies), PCDNA2.1 plasmid (Invitrogen,

Carlsbad CA), PBK-CMV plasmid (Stratagene), PCR2-TOPOTA plasmid (Invitrogen), PCMV-ICIS plasmid (Stratagene), pIGEN (Incyte Genomics, Palo Alto CA), pRARE (Incyte Genomics), or pINCY (Incyte Genomics), or derivatives thereof. Recombinant plasmids were transformed into competent *E. coli* cells including XL1-Blue, XL1-BlueMRF, or SOLR from Stratagene or DH5 $\alpha$ ,  
5 DH10B, or ElectroMAX DH10B from Life Technologies.

## II. Isolation of cDNA Clones

Plasmids were recovered from host cells by *in vivo* excision using the UNIZAP vector system (Stratagene) or by cell lysis. Plasmids were purified using at least one of the following: the Magic or  
10 WIZARD Minipreps DNA purification system (Promega); the AGTC Miniprep purification kit (Edge BioSystems, Gaithersburg MD); and the QIAWELL 8, QIAWELL 8 Plus, and QIAWELL 8 Ultra plasmid purification systems or the R.E.A.L. PREP 96 plasmid purification kit (QIAGEN). Following precipitation, plasmids were resuspended in 0.1 ml of distilled water and stored, with or without lyophilization, at 4°C.

15 Alternatively, plasmid DNA was amplified from host cell lysates using direct link PCR in a high-throughput format. (Rao, V.B. (1994) Anal. Biochem. 216:1-14.) Host cell lysis and thermal cycling steps were carried out in a single reaction mixture. Samples were processed and stored in 384-well plates, and the concentration of amplified plasmid DNA was quantified fluorometrically using PICOGREEN dye (Molecular Probes, Inc. (Molecular Probes), Eugene OR) and a FLUOROSKAN  
20 II fluorescence scanner (Labsystems Oy, Helsinki, Finland).

## III. Sequencing and Analysis

cDNA sequencing reactions were processed using standard methods or high-throughput instrumentation such as the ABI CATALYST 800 thermal cycler (Applied Biosystems) or the PTC-  
25 200 thermal cycler (MJ Research) in conjunction with the HYDRA microdispenser (Robbins Scientific Corp., Sunnyvale CA) or the MICROLAB 2200 liquid transfer system (Hamilton). cDNA sequencing reactions were prepared using reagents provided by Amersham Pharmacia Biotech or supplied in ABI sequencing kits such as the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Applied Biosystems). Electrophoretic separation of cDNA sequencing reactions  
30 and detection of labeled polynucleotides were carried out using the MEGABACE 1000 DNA sequencing system (Molecular Dynamics); the ABI PRISM 373 or 377 sequencing system (Applied Biosystems) in conjunction with standard ABI protocols and base calling software; or other sequence analysis systems known in the art. Reading frames within the cDNA sequences were identified using standard methods (reviewed in Ausubel, 1997, *supra*, Chapter 7.7). Some of the cDNA sequences

were selected for extension using the techniques disclosed in Example VIII.

#### **IV. Assembly and Analysis of Sequences**

Component sequences from chromatograms were subject to PHRED analysis and assigned a quality score. The sequences having at least a required quality score were subject to various pre-processing editing pathways to eliminate, e.g., low quality 3' ends, vector and linker sequences, polyA tails, Alu repeats, mitochondrial and ribosomal sequences, bacterial contamination sequences, and sequences smaller than 50 base pairs. In particular, low-information sequences and repetitive elements (e.g., dinucleotide repeats, Alu repeats, etc.) were replaced by "n's", or masked, to prevent spurious matches.

Processed sequences were then subject to assembly procedures in which the sequences were assigned to gene bins (bins). Each sequence could only belong to one bin. Sequences in each gene bin were assembled to produce consensus sequences (templates). Subsequent new sequences were added to existing bins using BLASTN (v.1.4 WashU) and CROSSMATCH. Candidate pairs were identified as all BLAST hits having a quality score greater than or equal to 150. Alignments of at least 82% local identity were accepted into the bin. The component sequences from each bin were assembled using a version of PHRAP. Bins with several overlapping component sequences were assembled using DEEP PHRAP. The orientation (sense or antisense) of each assembled template was determined based on the number and orientation of its component sequences. Template sequences as disclosed in the sequence listing correspond to sense strand sequences (the "forward" reading frames), to the best determination. The complementary (antisense) strands are inherently disclosed herein. The component sequences which were used to assemble each template consensus sequence are listed in Table 5, along with their positions along the template nucleotide sequences.

Bins were compared against each other and those having local similarity of at least 82% were combined and reassembled. Reassembled bins having templates of insufficient overlap (less than 95% local identity) were re-split. Assembled templates were also subject to analysis by STITCHER/EXON MAPPER algorithms which analyze the probabilities of the presence of splice variants, alternatively spliced exons, splice junctions, differential expression of alternative spliced genes across tissue types or disease states, etc. These resulting bins were subject to several rounds of the above assembly procedures.

Once gene bins were generated based upon sequence alignments, bins were clone joined based upon clone information. If the 5' sequence of one clone was present in one bin and the 3' sequence from the same clone was present in a different bin, it was likely that the two bins actually belonged together in a single bin. The resulting combined bins underwent assembly procedures to regenerate the consensus sequences.

The final assembled templates were subsequently annotated using the following procedure. Template sequences were analyzed using BLASTN (v2.0, NCBI) versus gbpri (GenBank version 128). "Hits" were defined as an exact match having from 95% local identity over 200 base pairs through 100% local identity over 100 base pairs, or a homolog match having an E-value, i.e. a probability score, of  $\leq 1 \times 10^{-8}$ . The hits were subject to frameshift FASTx versus GENPEPT (GenBank version 128). (See Table 8). In this analysis, a homolog match was defined as having an E-value of  $\leq 1 \times 10^{-8}$ . The assembly method used above was described in "System and Methods for Analyzing Biomolecular Sequences," U.S.S.N. 09/276,534, filed March 25, 1999, and the LIFESEQ Gold user manual (Incyte) both incorporated by reference herein.

Following assembly, template sequences were subjected to motif, BLAST, and functional analyses, and categorized in protein hierarchies using methods described in, e.g., "Database System Employing Protein Function Hierarchies for Viewing Biomolecular Sequence Data," U.S. Patent Number 6,023,659; "Relational Database for Storing Biomolecule Information," U.S.S.N. 08/947,845, filed October 9, 1997; "Project-Based Full-Length Biomolecular Sequence Database," U.S. Patent Number 5,953,727, filed March 6, 1997; and "Relational Database and System for Storing Information Relating to Biomolecular Sequences," U.S.S.N. 09/034,807, filed March 4, 1998, all of which are incorporated by reference herein.

The template sequences were further analyzed by translating each template in all three forward reading frames and searching each translation against the Pfam database of hidden Markov model-based protein families and domains using the HMMER software package (available to the public from Washington University School of Medicine, St. Louis MO). Regions of templates which, when translated, contain similarity to Pfam consensus sequences are reported in Table 3, along with descriptions of Pfam protein domains and families. Only those Pfam hits with an E-value of  $\leq 1 \times 10^{-3}$  are reported. (See also World Wide Web site <http://pfam.wustl.edu/> for detailed descriptions of Pfam protein domains and families.)

Additionally, the template sequences were translated in all three forward reading frames, and each translation was searched against hidden Markov models for signal peptides using the HMMER software package. Construction of hidden Markov models and their usage in sequence analysis has been described. (See, for example, Eddy, S.R. (1996) Curr. Opin. Str. Biol. 6:361-365.) Only those signal peptide hits with a cutoff score of 11 bits or greater are reported. A cutoff score of 11 bits or greater corresponds to at least about 91-94% true-positives in signal peptide prediction. Template sequences were also translated in all three forward reading frames, and each translation was searched against TMHMMER, a program that uses a hidden Markov model (HMM) to delineate transmembrane segments on protein sequences and determine orientation (Sonnhammer, E.L. et al.

(1998) Proc. Sixth Intl. Conf. On Intelligent Systems for Mol. Biol., Glasgow et al., eds., The Am. Assoc. for Artificial Intelligence (AAAI) Press, Menlo Park, CA, and MIT Press, Cambridge, MA, pp. 175-182.) Regions of templates which, when translated, contain similarity to signal peptide or transmembrane consensus sequences are reported in Table 4.

5        The results of HMMER analysis as reported in Tables 3 and 4 may support the results of BLAST analysis as reported in Table 2 or may suggest alternative or additional properties of template-encoded polypeptides not previously uncovered by BLAST or other analyses.

10        Template sequences are further analyzed using the bioinformatics tools listed in Table 8, or using sequence analysis software known in the art such as MACDNASIS PRO software (Hitachi Software Engineering, South San Francisco CA) and LASERGENE software (DNASTAR). Template sequences may be further queried against public databases such as the GenBank rodent, mammalian, vertebrate, prokaryote, and eukaryote databases.

15        The template sequences were translated to derive the corresponding longest open reading frame as presented by the polypeptide sequences as reported in Table 7. Alternatively, a polypeptide of the invention may begin at any of the methionine residues within the full length translated polypeptide. Polypeptide sequences were subsequently analyzed by querying against the GenBank protein database (GENPEPT, (GenBank version 128)). Full length polynucleotide sequences are also analyzed using MACDNASIS PRO software (Hitachi Software Engineering, South San Francisco CA) and LASERGENE software (DNASTAR). Polynucleotide and polypeptide sequence alignments  
20        are generated using default parameters specified by the CLUSTAL algorithm as incorporated into the MEGALIGN multisequence alignment program (DNASTAR), which also calculates the percent identity between aligned sequences.

25        Table 7 shows sequences with homology to the polypeptides of the invention as identified by BLAST analysis against the GenBank protein (GENPEPT) database. Column 1 shows the polypeptide sequence identification number (SEQ ID NO:) for the polypeptide segments of the invention. Column 2 shows the reading frame used in the translation of the polynucleotide sequences encoding the polypeptide segments. Column 3 shows the length of the translated polypeptide segments. Columns 4 and 5 show the start and stop nucleotide positions of the polynucleotide sequences encoding the polypeptide segments. Column 6 shows the GenBank identification number  
30        (GI Number) of the nearest GenBank homolog. Column 7 shows the probability score for the match between each polypeptide and its GenBank homolog. Column 8 shows the annotation of the GenBank homolog.

## **V. Analysis of Polynucleotide Expression**



Northern analysis is a laboratory technique used to detect the presence of a transcript of a gene and involves the hybridization of a labeled nucleotide sequence to a membrane on which RNAs from a particular cell type or tissue have been bound. (See, e.g., Sambrook, supra, ch. 7; Ausubel, 1995, supra, ch. 4 and 16.)

5 Analogous computer techniques applying BLAST were used to search for identical or related molecules in cDNA databases such as GenBank or LIFESEQ (Incyte Genomics). This analysis is much faster than multiple membrane-based hybridizations. In addition, the sensitivity of the computer search can be modified to determine whether any particular match is categorized as exact or similar. The basis of the search is the product score, which is defined as:

10

$$\frac{\text{BLAST Score} \times \text{Percent Identity}}{5 \times \text{minimum} \{ \text{length}(\text{Seq. 1}), \text{length}(\text{Seq. 2}) \}}$$

The product score takes into account both the degree of similarity between two sequences and the  
15 length of the sequence match. The product score is a normalized value between 0 and 100, and is calculated as follows: the BLAST score is multiplied by the percent nucleotide identity and the product is divided by (5 times the length of the shorter of the two sequences). The BLAST score is calculated by assigning a score of +5 for every base that matches in a high-scoring segment pair (HSP), and -4 for every mismatch. Two sequences may share more than one HSP (separated by  
20 gaps). If there is more than one HSP, then the pair with the highest BLAST score is used to calculate the product score. The product score represents a balance between fractional overlap and quality in a BLAST alignment. For example, a product score of 100 is produced only for 100% identity over the entire length of the shorter of the two sequences being compared. A product score of 70 is produced either by 100% identity and 70% overlap at one end, or by 88% identity and 100% overlap at the  
25 other. A product score of 50 is produced either by 100% identity and 50% overlap at one end, or 79% identity and 100% overlap.

## VI. Tissue Distribution Profiling

A tissue distribution profile is determined for each template by compiling the cDNA library  
30 tissue classifications of its component cDNA sequences. Each component sequence, is derived from a cDNA library constructed from a human tissue. Each human tissue is classified into one of the following categories: cardiovascular system; connective tissue; digestive system; embryonic structures; endocrine system; exocrine glands; genitalia, female; genitalia, male; germ cells; hemic and immune system; liver; musculoskeletal system; nervous system; pancreas; respiratory system; sense  
35 organs; skin; stomatognathic system; unclassified/mixed; or urinary tract. Template sequences,

component sequences, and cDNA library/tissue information are found in the LIFESEQ GOLD database (Incyte Genomics, Palo Alto CA).

Table 6 shows the tissue distribution profile for the templates of the invention. For each template, the three most frequently observed tissue categories are shown in column 3, along with the percentage of component sequences belonging to each category. Only tissue categories with percentage values of  $\geq 10\%$  are shown. A tissue distribution of "widely distributed" in column 3 indicates percentage values of  $<10\%$  in all tissue categories.

## **VII. Transcript Image Analysis**

Transcript images are generated as described in Seilhamer et al., "Comparative Gene Transcript Analysis," U.S. Patent Number 5,840,484, incorporated herein by reference.

## **VIII. Extension of Polynucleotide Sequences and Isolation of a Full-length cDNA**

Oligonucleotide primers designed using an mddt of the Sequence Listing are used to extend the nucleic acid sequence. One primer is synthesized to initiate 5' extension of the template, and the other primer, to initiate 3' extension of the template. The initial primers may be designed using OLIGO 4.06 software (National Biosciences, Inc. (National Biosciences), Plymouth MN), or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the target sequence at temperatures of about 68°C to about 72°C. Any stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations are avoided. Selected human cDNA libraries are used to extend the sequence. If more than one extension is necessary or desired, additional or nested sets of primers are designed.

High fidelity amplification is obtained by PCR using methods well known in the art. PCR is performed in 96-well plates using the PTC-200 thermal cycler (MJ Research). The reaction mix contains DNA template, 200 nmol of each primer, reaction buffer containing  $Mg^{2+}$ ,  $(NH_4)_2SO_4$ , and  $\beta$ -mercaptoethanol, Taq DNA polymerase (Amersham Pharmacia Biotech), ELONGASE enzyme (Life Technologies), and Pfu DNA polymerase (Stratagene), with the following parameters for primer pair PCI A and PCI B: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C. In the alternative, the parameters for primer pair T7 and SK+ are as follows: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 57°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C.

The concentration of DNA in each well is determined by dispensing 100  $\mu$ l PICOGREEN quantitation reagent (0.25% (v/v); Molecular Probes) dissolved in 1X Tris-EDTA (TE) and 0.5  $\mu$ l of undiluted PCR product into each well of an opaque fluorimeter plate (Corning Incorporated (Corning),

Corning NY), allowing the DNA to bind to the reagent. The plate is scanned in a FLUOROSKAN II (Labsystems Oy) to measure the fluorescence of the sample and to quantify the concentration of DNA. A 5  $\mu$ l to 10  $\mu$ l aliquot of the reaction mixture is analyzed by electrophoresis on a 1 % agarose mini-gel to determine which reactions are successful in extending the sequence.

5           The extended nucleotides are desalted and concentrated, transferred to 384-well plates, digested with CviJI cholera virus endonuclease (Molecular Biology Research, Madison WI), and sonicated or sheared prior to religation into pUC 18 vector (Amersham Pharmacia Biotech). For shotgun sequencing, the digested nucleotides are separated on low concentration (0.6 to 0.8%) agarose gels, fragments are excised, and agar digested with AGAR ACE (Promega). Extended  
10 clones are religated using T4 ligase (New England Biolabs, Inc., Beverly MA) into pUC 18 vector (Amersham Pharmacia Biotech), treated with Pfu DNA polymerase (Stratagene) to fill-in restriction site overhangs, and transfected into competent *E. coli* cells. Transformed cells are selected on antibiotic-containing media, individual colonies are picked and cultured overnight at 37°C in 384-well plates in LB/2x carbenicillin liquid media.

15           The cells are lysed, and DNA is amplified by PCR using Taq DNA polymerase (Amersham Pharmacia Biotech) and Pfu DNA polymerase (Stratagene) with the following parameters: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 72°C, 2 min; Step 5: steps 2, 3, and 4 repeated 29 times; Step 6: 72°C, 5 min; Step 7: storage at 4°C. DNA is quantified by PICOGREEN reagent (Molecular Probes) as described above. Samples with low DNA recoveries are reamplified  
20 using the same conditions as described above. Samples are diluted with 20% dimethylsulfoxide (1:2, v/v), and sequenced using DYENAMIC energy transfer sequencing primers and the DYENAMIC DIRECT kit (Amersham Pharmacia Biotech) or the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Applied Biosystems).

          In like manner, the mddt is used to obtain regulatory sequences (promoters, introns, and  
25 enhancers) using the procedure above, oligonucleotides designed for such extension, and an appropriate genomic library.

## **IX.     Labeling of Probes and Southern Hybridization Analyses**

          Hybridization probes derived from the mddt of the Sequence Listing are employed for  
30 screening cDNAs, mRNAs, or genomic DNA. The labeling of probe nucleotides between 100 and 1000 nucleotides in length is specifically described, but essentially the same procedure may be used with larger cDNA fragments. Probe sequences are labeled at room temperature for 30 minutes using a T4 polynucleotide kinase,  $\gamma^{32}\text{P}$ -ATP, and 0.5X One-Phor-All Plus (Amersham Pharmacia Biotech) buffer and purified using a ProbeQuant G-50 Microcolumn (Amersham Pharmacia Biotech). The

probe mixture is diluted to  $10^7$  dpm/ $\mu$ g/ml hybridization buffer and used in a typical membrane-based hybridization analysis.

The DNA is digested with a restriction endonuclease such as Eco RV and is electrophoresed through a 0.7% agarose gel. The DNA fragments are transferred from the agarose to nylon  
5 membrane (NYTRAN Plus, Schleicher & Schuell, Inc., Keene NH) using procedures specified by the manufacturer of the membrane. Prehybridization is carried out for three or more hours at 68°C, and hybridization is carried out overnight at 68°C. To remove non-specific signals, blots are sequentially washed at room temperature under increasingly stringent conditions, up to 0.1x saline sodium citrate (SSC) and 0.5% sodium dodecyl sulfate. After the blots are placed in a PHOSPHORIMAGER  
10 cassette (Molecular Dynamics) or are exposed to autoradiography film, hybridization patterns of standard and experimental lanes are compared. Essentially the same procedure is employed when screening RNA.

#### **X. Chromosome Mapping of mddt**

15 The cDNA sequences which were used to assemble SEQ ID NO:1-396 are compared with sequences from the Incyte LIFESEQ database and public domain databases using BLAST and other implementations of the Smith-Waterman algorithm. Sequences from these databases that match SEQ ID NO:1-396 are assembled into clusters of contiguous and overlapping sequences using assembly algorithms such as PHRAP (Table 8). Radiation hybrid and genetic mapping data available from  
20 public resources such as the Stanford Human Genome Center (SHGC), Whitehead Institute for Genome Research (WIGR), and Généthon are used to determine if any of the clustered sequences have been previously mapped. Inclusion of a mapped sequence in a cluster will result in the assignment of all sequences of that cluster, including its particular SEQ ID NO:, to that map location. The genetic map locations of SEQ ID NO:1-396 are described as ranges, or intervals, of human  
25 chromosomes. The map position of an interval, in centiMorgans, is measured relative to the terminus of the chromosome's p-arm. (The centiMorgan (cM) is a unit of measurement based on recombination frequencies between chromosomal markers. On average, 1 cM is roughly equivalent to 1 megabase (Mb) of DNA in humans, although this can vary widely due to hot and cold spots of recombination.) The cM distances are based on genetic markers mapped by Généthon which provide  
30 boundaries for radiation hybrid markers whose sequences were included in each of the clusters.

#### **XI. Microarray Analysis**

##### **Probe Preparation from Tissue or Cell Samples**

Total RNA is isolated from tissue samples using the guanidinium thiocyanate method and  
35 polyA<sup>+</sup> RNA is purified using the oligo (dT) cellulose method. Each polyA<sup>+</sup> RNA sample is reverse

transcribed using MMLV reverse-transcriptase, 0.05 pg/ $\mu$ l oligo-dT primer (21mer), 1X first strand buffer, 0.03 units/ $\mu$ l RNase inhibitor, 500  $\mu$ M dATP, 500  $\mu$ M dGTP, 500  $\mu$ M dTTP, 40  $\mu$ M dCTP, 40  $\mu$ M dCTP-Cy3 (BDS) or dCTP-Cy5 (Amersham Pharmacia Biotech). The reverse transcription reaction is performed in a 25 ml volume containing 200 ng polyA<sup>+</sup> RNA with GEMBRIGHT kits (Incyte). Specific control polyA<sup>+</sup> RNAs are synthesized by in vitro transcription from non-coding yeast genomic DNA (W. Lei, unpublished). As quantitative controls, the control mRNAs at 0.002 ng, 0.02 ng, 0.2 ng, and 2 ng are diluted into reverse transcription reaction at ratios of 1:100,000, 1:10,000, 1:1000, 1:100 (w/w) to sample mRNA respectively. The control mRNAs are diluted into reverse transcription reaction at ratios of 1:3, 3:1, 1:10, 10:1, 1:25, 25:1 (w/w) to sample mRNA differential expression patterns. After incubation at 37°C for 2 hr, each reaction sample (one with Cy3 and another with Cy5 labeling) is treated with 2.5 ml of 0.5M sodium hydroxide and incubated for 20 minutes at 85°C to stop the reaction and degrade the RNA. Probes are purified using two successive CHROMA SPIN 30 gel filtration spin columns (CLONTECH Laboratories, Inc. (CLONTECH), Palo Alto CA) and after combining, both reaction samples are ethanol precipitated using 1 ml of glycogen (1 mg/ml), 60 ml sodium acetate, and 300 ml of 100% ethanol. The probe is then dried to completion using a SpeedVAC (Savant Instruments Inc., Holbrook NY) and resuspended in 14  $\mu$ l 5X SSC/0.2% SDS.

#### Microarray Preparation

Sequences of the present invention are used to generate array elements. Each array element is amplified from bacterial cells containing vectors with cloned cDNA inserts. PCR amplification uses primers complementary to the vector sequences flanking the cDNA insert. Array elements are amplified in thirty cycles of PCR from an initial quantity of 1-2 ng to a final quantity greater than 5  $\mu$ g. Amplified array elements are then purified using SEPHACRYL-400 (Amersham Pharmacia Biotech).

Purified array elements are immobilized on polymer-coated glass slides. Glass microscope slides (Corning) are cleaned by ultrasound in 0.1% SDS and acetone, with extensive distilled water washes between and after treatments. Glass slides are etched in 4% hydrofluoric acid (VWR Scientific Products Corporation (VWR), West Chester, PA), washed extensively in distilled water, and coated with 0.05% aminopropyl silane (Sigma) in 95% ethanol. Coated slides are cured in a 110°C oven.

Array elements are applied to the coated glass substrate using a procedure described in US Patent No. 5,807,522, incorporated herein by reference. 1  $\mu$ l of the array element DNA, at an average concentration of 100 ng/ $\mu$ l, is loaded into the open capillary printing element by a high-speed robotic apparatus. The apparatus then deposits about 5 nl of array element sample per slide.

Microarrays are UV-crosslinked using a STRATALINKER UV-crosslinker (Stratagene). Microarrays are washed at room temperature once in 0.2% SDS and three times in distilled water. Non-specific binding sites are blocked by incubation of microarrays in 0.2% casein in phosphate buffered saline (PBS) (Tropix, Inc., Bedford, MA) for 30 minutes at 60°C followed by washes in  
5 0.2% SDS and distilled water as before.

### Hybridization

Hybridization reactions contain 9 µl of probe mixture consisting of 0.2 µg each of Cy3 and Cy5 labeled cDNA synthesis products in 5X SSC, 0.2% SDS hybridization buffer. The probe mixture is  
10 heated to 65°C for 5 minutes and is aliquoted onto the microarray surface and covered with an 1.8 cm<sup>2</sup> coverslip. The arrays are transferred to a waterproof chamber having a cavity just slightly larger than a microscope slide. The chamber is kept at 100% humidity internally by the addition of 140 µl of 5x SSC in a corner of the chamber. The chamber containing the arrays is incubated for about 6.5 hours at 60°C. The arrays are washed for 10 min at 45°C in a first wash buffer (1X SSC, 0.1%  
15 SDS), three times for 10 minutes each at 45°C in a second wash buffer (0.1X SSC), and dried.

### Detection

Reporter-labeled hybridization complexes are detected with a microscope equipped with an Innova 70 mixed gas 10 W laser (Coherent, Inc., Santa Clara CA) capable of generating spectral lines  
20 at 488 nm for excitation of Cy3 and at 632 nm for excitation of Cy5. The excitation laser light is focused on the array using a 20X microscope objective (Nikon, Inc., Melville NY). The slide containing the array is placed on a computer-controlled X-Y stage on the microscope and raster-scanned past the objective. The 1.8 cm x 1.8 cm array used in the present example is scanned with a resolution of 20 micrometers.

In two separate scans, a mixed gas multiline laser excites the two fluorophores sequentially. Emitted light is split, based on wavelength, into two photomultiplier tube detectors (PMT R1477, Hamamatsu Photonics Systems, Bridgewater NJ) corresponding to the two fluorophores. Appropriate filters positioned between the array and the photomultiplier tubes are used to filter the signals. The emission maxima of the fluorophores used are 565 nm for Cy3 and 650 nm for Cy5. Each array is  
30 typically scanned twice, one scan per fluorophore using the appropriate filters at the laser source, although the apparatus is capable of recording the spectra from both fluorophores simultaneously.

The sensitivity of the scans is typically calibrated using the signal intensity generated by a cDNA control species added to the probe mix at a known concentration. A specific location on the array contains a complementary DNA sequence, allowing the intensity of the signal at that location to

be correlated with a weight ratio of hybridizing species of 1:100,000. When two probes from different sources (e.g., representing test and control cells), each labeled with a different fluorophore, are hybridized to a single array for the purpose of identifying genes that are differentially expressed, the calibration is done by labeling samples of the calibrating cDNA with the two fluorophores and  
5 adding identical amounts of each to the hybridization mixture.

The output of the photomultiplier tube is digitized using a 12-bit RTI-835H analog-to-digital (A/D) conversion board (Analog Devices, Inc., Norwood, MA) installed in an IBM-compatible PC computer. The digitized data are displayed as an image where the signal intensity is mapped using a linear 20-color transformation to a pseudocolor scale ranging from blue (low signal) to red (high  
10 signal). The data is also analyzed quantitatively. Where two different fluorophores are excited and measured simultaneously, the data are first corrected for optical crosstalk (due to overlapping emission spectra) between the fluorophores using each fluorophore's emission spectrum.

A grid is superimposed over the fluorescence signal image such that the signal from each spot is centered in each element of the grid. The fluorescence signal within each element is then  
15 integrated to obtain a numerical value corresponding to the average intensity of the signal. The software used for signal analysis is the GEMTOOLS gene expression analysis program (Incyte).

## **XII. Complementary Nucleic Acids**

Sequences complementary to the mddt are used to detect, decrease, or inhibit expression of  
20 the naturally occurring nucleotide. The use of oligonucleotides comprising from about 15 to 30 base pairs is typical in the art. However, smaller or larger sequence fragments can also be used. Appropriate oligonucleotides are designed from the mddt using OLIGO 4.06 software (National Biosciences) or other appropriate programs and are synthesized using methods standard in the art or ordered from a commercial supplier. To inhibit transcription, a complementary oligonucleotide is  
25 designed from the most unique 5' sequence and used to prevent transcription factor binding to the promoter sequence. To inhibit translation, a complementary oligonucleotide is designed to prevent ribosomal binding and processing of the transcript.

## **XIII. Expression of MDDT**

Expression and purification of MDDT is accomplished using bacterial or virus-based  
30 expression systems. For expression of MDDT in bacteria, cDNA is subcloned into an appropriate vector containing an antibiotic resistance gene and an inducible promoter that directs high levels of cDNA transcription. Examples of such promoters include, but are not limited to, the *trp-lac* (*tac*) hybrid promoter and the T5 or T7 bacteriophage promoter in conjunction with the *lac* operator regulatory element. Recombinant vectors are transformed into suitable bacterial hosts, e.g.,

BL21(DE3). Antibiotic resistant bacteria express MDDT upon induction with isopropyl beta-D-thiogalactopyranoside (IPTG). Expression of MDDT in eukaryotic cells is achieved by infecting insect or mammalian cell lines with recombinant Autographica californica nuclear polyhedrosis virus (AcMNPV), commonly known as baculovirus. The nonessential polyhedrin gene of baculovirus is replaced with cDNA encoding MDDT by either homologous recombination or bacterial-mediated transposition involving transfer plasmid intermediates. Viral infectivity is maintained and the strong polyhedrin promoter drives high levels of cDNA transcription. Recombinant baculovirus is used to infect Spodoptera frugiperda (Sf9) insect cells in most cases, or human hepatocytes, in some cases. Infection of the latter requires additional genetic modifications to baculovirus. (See e.g., Engelhard, supra; and Sandig, supra.)

In most expression systems, MDDT is synthesized as a fusion protein with, e.g., glutathione S-transferase (GST) or a peptide epitope tag, such as FLAG or 6-His, permitting rapid, single-step, affinity-based purification of recombinant fusion protein from crude cell lysates. GST, a 26-kilodalton enzyme from Schistosoma japonicum, enables the purification of fusion proteins on immobilized glutathione under conditions that maintain protein activity and antigenicity (Amersham Pharmacia Biotech). Following purification, the GST moiety can be proteolytically cleaved from MDDT at specifically engineered sites. FLAG, an 8-amino acid peptide, enables immunoaffinity purification using commercially available monoclonal and polyclonal anti-FLAG antibodies (Eastman Kodak Company, Rochester NY). 6-His, a stretch of six consecutive histidine residues, enables purification on metal-chelate resins (QIAGEN). Methods for protein expression and purification are discussed in Ausubel (1995, supra, Chapters 10 and 16). Purified MDDT obtained by these methods can be used directly in the following activity assay.

#### **XIV. Demonstration of MDDT Activity**

MDDT, or biologically active fragments thereof, are labeled with <sup>125</sup>I Bolton-Hunter reagent. (See, e.g., Bolton, A.E. and W.M. Hunter (1973) Biochem. J. 133:529-539.) Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled MDDT, washed, and any wells with labeled MDDT complex are assayed. Data obtained using different concentrations of MDDT are used to calculate values for the number, affinity, and association of MDDT with the candidate molecules.

Alternatively, molecules interacting with MDDT are analyzed using the yeast two-hybrid system as described in Fields, S. and O. Song (1989) Nature 340:245-246, or using commercially available kits based on the two-hybrid system, such as the MATCHMAKER system (CLONTECH).

MDDT may also be used in the PATHCALLING process (CuraGen Corp., New Haven CT) which employs the yeast two-hybrid system in a high-throughput manner to determine all interactions



between the proteins encoded by two large libraries of genes (Nandabalan, K. et al. (2000) U.S. Patent No. 6,057,101).

## **XV. Functional Assays**

MDDT function is assessed by expressing mddt at physiologically elevated levels in  
5 mammalian cell culture systems. cDNA is subcloned into a mammalian expression vector containing a strong promoter that drives high levels of cDNA expression. Vectors of choice include pCMV SPORT (Life Technologies) and pCR3.1 (Invitrogen Corporation, Carlsbad CA), both of which contain the cytomegalovirus promoter. 5-10  $\mu$ g of recombinant vector are transiently transfected into a human cell line, preferably of endothelial or hematopoietic origin, using either liposome formulations  
10 or electroporation. 1-2  $\mu$ g of an additional plasmid containing sequences encoding a marker protein are co-transfected.

Expression of a marker protein provides a means to distinguish transfected cells from nontransfected cells and is a reliable predictor of cDNA expression from the recombinant vector. Marker proteins of choice include, e.g., Green Fluorescent Protein (GFP; CLONTECH), CD64, or a  
15 CD64-GFP fusion protein. Flow cytometry (FCM), an automated laser optics-based technique, is used to identify transfected cells expressing GFP or CD64-GFP and to evaluate the apoptotic state of the cells and other cellular properties.

FCM detects and quantifies the uptake of fluorescent molecules that diagnose events preceding or coincident with cell death. These events include changes in nuclear DNA content as  
20 measured by staining of DNA with propidium iodide; changes in cell size and granularity as measured by forward light scatter and 90 degree side light scatter; down-regulation of DNA synthesis as measured by decrease in bromodeoxyuridine uptake; alterations in expression of cell surface and intracellular proteins as measured by reactivity with specific antibodies; and alterations in plasma membrane composition as measured by the binding of fluorescein-conjugated Annexin V protein to the  
25 cell surface. Methods in flow cytometry are discussed in Ormerod, M. G. (1994) Flow Cytometry, Oxford, New York NY.

The influence of MDDT on gene expression can be assessed using highly purified populations of cells transfected with sequences encoding MDDT and either CD64 or CD64-GFP. CD64 and CD64-GFP are expressed on the surface of transfected cells and bind to conserved regions of human  
30 immunoglobulin G (IgG). Transfected cells are efficiently separated from nontransfected cells using magnetic beads coated with either human IgG or antibody against CD64 (DYNAL, Inc., Lake Success NY). mRNA can be purified from the cells using methods well known by those of skill in the art. Expression of mRNA encoding MDDT and other genes of interest can be analyzed by northern analysis or microarray techniques.

## **35 XVI. Production of Antibodies**

MDDT substantially purified using polyacrylamide gel electrophoresis (PAGE; see, e.g., Harrington, M.G. (1990) *Methods Enzymol.* 182:488-495), or other purification techniques, is used to immunize rabbits and to produce antibodies using standard protocols.

Alternatively, the MDDT amino acid sequence is analyzed using LASERGENE software (DNASTAR) to determine regions of high immunogenicity, and a corresponding peptide is synthesized and used to raise antibodies by means known to those of skill in the art. Methods for selection of appropriate epitopes, such as those near the C-terminus or in hydrophilic regions are well described in the art. (See, e.g., Ausubel, 1995, *supra*, Chapter 11.)

Typically, peptides 15 residues in length are synthesized using an ABI 431A peptide synthesizer (Applied Biosystems) using fmoc-chemistry and coupled to KLH (Sigma) by reaction with N-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS) to increase immunogenicity. (See, e.g., Ausubel, *supra*.) Rabbits are immunized with the peptide-KLH complex in complete Freund's adjuvant. Resulting antisera are tested for anti-peptide activity by, for example, binding the peptide to plastic, blocking with 1% BSA, reacting with rabbit antisera, washing, and reacting with radio-iodinated goat anti-rabbit IgG. Antisera with anti-peptide activity are tested for anti-MDDT activity using protocols well known in the art, including ELISA, RIA, and immunoblotting.

#### **XVII. Purification of Naturally Occurring MDDT Using Specific Antibodies**

Naturally occurring or recombinant MDDT is substantially purified by immunoaffinity chromatography using antibodies specific for MDDT. An immunoaffinity column is constructed by covalently coupling anti-MDDT antibody to an activated chromatographic resin, such as CNBr-activated SEPHAROSE (Amersham Pharmacia Biotech). After the coupling, the resin is blocked and washed according to the manufacturer's instructions.

Media containing MDDT are passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of MDDT (e.g., high ionic strength buffers in the presence of detergent). The column is eluted under conditions that disrupt antibody/MDDT binding (e.g., a buffer of pH 2 to pH 3, or a high concentration of a chaotrope, such as urea or thiocyanate ion), and MDDT is collected.

All publications and patents mentioned in the above specification are herein incorporated by reference. Various modifications and variations of the described method and system of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the above-described modes for carrying out the invention which are obvious to those skilled in the field of molecular biology or related fields are intended to be within the scope of the following claims.

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
1	LG:036272.1:2001MAR30	397	LG:036272.1.orf2:2001MAR30
2	LG:093337.3:2001MAR30	398	LG:093337.3.orf2:2001MAR30
3	LG:1049927.6:2001MAR30	399	LG:1049927.6.orf3:2001MAR30
4	LG:1051891.34:2001MAR30	400	LG:1051891.34.orf1:2001MAR30
5	LG:1089626.1:2001MAR30	401	LG:1089626.1.orf3:2001MAR30
6	LG:1101416.6:2001MAR30	402	LG:1101416.6.orf2:2001MAR30
7	LG:1295974.1:2001MAR30	403	LG:1295974.1.orf2:2001MAR30
8	LG:1400572.2:2001MAR30	404	LG:1400572.2.orf1:2001MAR30
9	LG:1446621.1:2001MAR30	405	LG:1446621.1.orf3:2001MAR30
10	LG:1499752.1:2001MAR30	406	LG:1499752.1.orf3:2001MAR30
11	LG:1503044.7:2001MAR30	407	LG:1503044.7.orf1:2001MAR30
12	LG:1503588.1:2001MAR30	408	LG:1503588.1.orf1:2001MAR30
13	LG:1503589.2:2001MAR30	409	LG:1503589.2.orf3:2001MAR30
14	LG:1506339.4:2001MAR30	410	LG:1506339.4.orf2:2001MAR30
15	LG:220648.6:2001MAR30	411	LG:220648.6.orf3:2001MAR30
16	LG:236654.1:2001MAR30	412	LG:236654.1.orf1:2001MAR30
17	LG:237699.26:2001MAR30	413	LG:237699.26.orf3:2001MAR30
18	LG:311541.16:2001MAR30	414	LG:311541.16.orf2:2001MAR30
19	LG:335923.7:2001MAR30	415	LG:335923.7.orf2:2001MAR30
20	LG:350342.14:2001MAR30	416	LG:350342.14.orf3:2001MAR30
21	LG:369301.32:2001MAR30	417	LG:369301.32.orf1:2001MAR30
22	LG:452089.1:2001MAR30	418	LG:452089.1.orf2:2001MAR30
23	LG:454087.3:2001MAR30	419	LG:454087.3.orf1:2001MAR30
24	LG:466302.1:2001MAR30	420	LG:466302.1.orf1:2001MAR30
25	LG:474267.1:2001MAR30	421	LG:474267.1.orf3:2001MAR30
26	LG:995613.10:2001MAR30	422	LG:995613.10.orf1:2001MAR30
27	LG:011843.5:2001MAR30	423	LG:011843.5.orf3:2001MAR30
28	LG:075904.32:2001MAR30	424	LG:075904.32.orf2:2001MAR30
29	LG:1004781.3:2001MAR30	425	LG:1004781.3.orf1:2001MAR30
30	LG:1041807.8:2001MAR30	426	LG:1041807.8.orf1:2001MAR30
31	LG:1044448.2:2001MAR30	427	LG:1044448.2.orf3:2001MAR30
32	LG:1080598.9:2001MAR30	428	LG:1080598.9.orf3:2001MAR30
33	LG:1081017.1:2001MAR30	429	LG:1081017.1.orf2:2001MAR30
34	LG:1083120.2:2001MAR30	430	LG:1083120.2.orf2:2001MAR30
35	LG:1097492.12:2001MAR30	431	LG:1097492.12.orf2:2001MAR30
36	LG:118834.9:2001MAR30	432	LG:118834.9.orf1:2001MAR30
37	LG:1227408.25:2001MAR30	433	LG:1227408.25.orf3:2001MAR30
38	LG:1326953.1:2001MAR30	434	LG:1326953.1.orf1:2001MAR30
39	LG:1397821.17:2001MAR30	435	LG:1397821.17.orf3:2001MAR30
40	LG:1512507.1:2001MAR30	436	LG:1512507.1.orf2:2001MAR30
41	LG:196583.5:2001MAR30	437	LG:196583.5.orf2:2001MAR30
42	LG:198669.1:2001MAR30	438	LG:198669.1.orf3:2001MAR30
43	LG:202943.1:2001MAR30	439	LG:202943.1.orf1:2001MAR30
44	LG:204724.3:2001MAR30	440	LG:204724.3.orf2:2001MAR30
45	LG:206425.10:2001MAR30	441	LG:206425.10.orf1:2001MAR30
46	LG:208190.2:2001MAR30	442	LG:208190.2.orf1:2001MAR30
47	LG:222927.2:2001MAR30	443	LG:222927.2.orf1:2001MAR30
48	LG:228046.5:2001MAR30	444	LG:228046.5.orf3:2001MAR30
49	LG:230980.1:2001MAR30	445	LG:230980.1.orf1:2001MAR30
50	LG:236976.2:2001MAR30	446	LG:236976.2.orf3:2001MAR30

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
51	LG:238322.6:2001MAR30	447	LG:238322.6.orf1:2001MAR30
52	LG:341461.1:2001MAR30	448	LG:341461.1.orf3:2001MAR30
53	LG:354088.1:2001MAR30	449	LG:354088.1.orf1:2001MAR30
54	LG:376275.1:2001MAR30	450	LG:376275.1.orf3:2001MAR30
55	LG:399281.3:2001MAR30	451	LG:399281.3.orf3:2001MAR30
56	LG:404921.10:2001MAR30	452	LG:404921.10.orf2:2001MAR30
57	LG:444677.34:2001MAR30	453	LG:444677.34.orf1:2001MAR30
58	LG:968691.1:2001MAR30	454	LG:968691.1.orf1:2001MAR30
59	LG:983862.1:2001MAR30	455	LG:983862.1.orf1:2001MAR30
60	LG:984130.1:2001MAR30	456	LG:984130.1.orf2:2001MAR30
61	LG:986291.1:2001MAR30	457	LG:986291.1.orf1:2001MAR30
62	LG:045210.8:2001MAR30	458	LG:045210.8.orf1:2001MAR30
63	LG:229284.39:2001MAR30	459	LG:229284.39.orf3:2001MAR30
64	LG:337810.20:2001MAR30	460	LG:337810.20.orf2:2001MAR30
65	LG:463420.1:2001MAR30	461	LG:463420.1.orf2:2001MAR30
66	LG:1080918.1:2001MAR30	462	LG:1080918.1.orf1:2001MAR30
67	LG:1093747.15:2001MAR30	463	LG:1093747.15.orf3:2001MAR30
68	LG:1096896.47:2001MAR30	464	LG:1096896.47.orf2:2001MAR30
69	LG:1098931.39:2001MAR30	465	LG:1098931.39.orf2:2001MAR30
70	LG:1100823.1:2001MAR30	466	LG:1100823.1.orf1:2001MAR30
71	LG:1166387.1:2001MAR30	467	LG:1166387.1.orf2:2001MAR30
72	LG:1383036.49:2001MAR30	468	LG:1383036.49.orf3:2001MAR30
73	LG:1452353.14:2001MAR30	469	LG:1452353.14.orf2:2001MAR30
74	LG:1452435.15:2001MAR30	470	LG:1452435.15.orf3:2001MAR30
75	LG:1498774.1:2001MAR30	471	LG:1498774.1.orf2:2001MAR30
76	LG:197180.1:2001MAR30	472	LG:197180.1.orf3:2001MAR30
77	LG:199489.1:2001MAR30	473	LG:199489.1.orf2:2001MAR30
78	LG:201908.3:2001MAR30	474	LG:201908.3.orf1:2001MAR30
79	LG:247245.26:2001MAR30	475	LG:247245.26.orf2:2001MAR30
80	LG:256365.2:2001MAR30	476	LG:256365.2.orf3:2001MAR30
81	LG:332923.4:2001MAR30	477	LG:332923.4.orf3:2001MAR30
82	LG:335276.1:2001MAR30	478	LG:335276.1.orf3:2001MAR30
83	LG:350272.2:2001MAR30	479	LG:350272.2.orf1:2001MAR30
84	LG:350921.2:2001MAR30	480	LG:350921.2.orf2:2001MAR30
85	LG:406568.1:2001MAR30	481	LG:406568.1.orf1:2001MAR30
86	LG:411043.3:2001MAR30	482	LG:411043.3.orf3:2001MAR30
87	LG:414376.20:2001MAR30	483	LG:414376.20.orf2:2001MAR30
88	LG:457695.1:2001MAR30	484	LG:457695.1.orf2:2001MAR30
89	LG:902390.2:2001MAR30	485	LG:902390.2.orf2:2001MAR30
90	LG:903565.20:2001MAR30	486	LG:903565.20.orf1:2001MAR30
91	LG:978182.4:2001MAR30	487	LG:978182.4.orf2:2001MAR30
92	LG:986827.1:2001MAR30	488	LG:986827.1.orf2:2001MAR30
93	LG:013792.1:2001MAR30	489	LG:013792.1.orf2:2001MAR30
94	LG:018258.1:2001MAR30	490	LG:018258.1.orf2:2001MAR30
95	LG:023126.3:2001MAR30	491	LG:023126.3.orf3:2001MAR30
96	LG:023618.1:2001MAR30	492	LG:023618.1.orf3:2001MAR30
97	LG:030999.1:2001MAR30	493	LG:030999.1.orf1:2001MAR30
98	LG:103508.1:2001MAR30	494	LG:103508.1.orf3:2001MAR30
99	LG:107976.15:2001MAR30	495	LG:107976.15.orf2:2001MAR30
100	LG:1080096.1:2001MAR30	496	LG:1080096.1.orf1:2001MAR30

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
101	LG:1080275.1:2001MAR30	497	LG:1080275.1.orf1:2001MAR30
102	LG:1090358.10:2001MAR30	498	LG:1090358.10.orf1:2001MAR30
103	LG:1095833.9:2001MAR30	499	LG:1095833.9.orf2:2001MAR30
104	LG:1383121.25:2001MAR30	500	LG:1383121.25.orf1:2001MAR30
105	LG:1386609.2:2001MAR30	501	LG:1386609.2.orf2:2001MAR30
106	LG:1398465.1:2001MAR30	502	LG:1398465.1.orf1:2001MAR30
107	LG:1453417.10:2001MAR30	503	LG:1453417.10.orf2:2001MAR30
108	LG:147869.3:2001MAR30	504	LG:147869.3.orf1:2001MAR30
109	LG:148485.5:2001MAR30	505	LG:148485.5.orf3:2001MAR30
110	LG:1501818.12:2001MAR30	506	LG:1501818.12.orf3:2001MAR30
111	LG:1508275.1:2001MAR30	507	LG:1508275.1.orf2:2001MAR30
112	LG:1509771.1:2001MAR30	508	LG:1509771.1.orf1:2001MAR30
113	LG:1512998.13:2001MAR30	509	LG:1512998.13.orf1:2001MAR30
114	LG:198251.7:2001MAR30	510	LG:198251.7.orf1:2001MAR30
115	LG:198296.1:2001MAR30	511	LG:198296.1.orf1:2001MAR30
116	LG:198876.13:2001MAR30	512	LG:198876.13.orf1:2001MAR30
117	LG:200704.1:2001MAR30	513	LG:200704.1.orf2:2001MAR30
118	LG:206593.3:2001MAR30	514	LG:206593.3.orf2:2001MAR30
119	LG:223970.11:2001MAR30	515	LG:223970.11.orf3:2001MAR30
120	LG:227500.5:2001MAR30	516	LG:227500.5.orf2:2001MAR30
121	LG:227722.7:2001MAR30	517	LG:227722.7.orf2:2001MAR30
122	LG:229105.1:2001MAR30	518	LG:229105.1.orf3:2001MAR30
123	LG:233761.4:2001MAR30	519	LG:233761.4.orf3:2001MAR30
124	LG:234326.67:2001MAR30	520	LG:234326.67.orf2:2001MAR30
125	LG:236056.27:2001MAR30	521	LG:236056.27.orf1:2001MAR30
126	LG:253889.31:2001MAR30	522	LG:253889.31.orf2:2001MAR30
127	LG:270833.135:2001MAR30	523	LG:270833.135.orf1:2001MAR30
128	LG:292613.7:2001MAR30	524	LG:292613.7.orf3:2001MAR30
129	LG:331546.2:2001MAR30	525	LG:331546.2.orf1:2001MAR30
130	LG:332027.6:2001MAR30	526	LG:332027.6.orf3:2001MAR30
131	LG:336998.1:2001MAR30	527	LG:336998.1.orf3:2001MAR30
132	LG:338010.8:2001MAR30	528	LG:338010.8.orf2:2001MAR30
133	LG:344597.1:2001MAR30	529	LG:344597.1.orf1:2001MAR30
134	LG:347361.2:2001MAR30	530	LG:347361.2.orf1:2001MAR30
135	LG:349293.17:2001MAR30	531	LG:349293.17.orf3:2001MAR30
136	LG:410595.19:2001MAR30	532	LG:410595.19.orf1:2001MAR30
137	LG:411151.35:2001MAR30	533	LG:411151.35.orf3:2001MAR30
138	LG:411334.8:2001MAR30	534	LG:411334.8.orf3:2001MAR30
139	LG:458583.1:2001MAR30	535	LG:458583.1.orf1:2001MAR30
140	LG:475378.1:2001MAR30	536	LG:475378.1.orf1:2001MAR30
141	LG:481572.1:2001MAR30	537	LG:481572.1.orf1:2001MAR30
142	LG:481704.1:2001MAR30	538	LG:481704.1.orf3:2001MAR30
143	LG:898195.4:2001MAR30	539	LG:898195.4.orf2:2001MAR30
144	LG:903785.1:2001MAR30	540	LG:903785.1.orf3:2001MAR30
145	LG:977454.3:2001MAR30	541	LG:977454.3.orf1:2001MAR30
146	LG:977724.12:2001MAR30	542	LG:977724.12.orf1:2001MAR30
147	LG:978215.19:2001MAR30	543	LG:978215.19.orf3:2001MAR30
148	LG:981795.1:2001MAR30	544	LG:981795.1.orf1:2001MAR30
149	LG:982784.1:2001MAR30	545	LG:982784.1.orf3:2001MAR30
150	LG:987322.4:2001MAR30	546	LG:987322.4.orf2:2001MAR30

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
151	LG:006242.7:2001MAR30	547	LG:006242.7.orf3:2001MAR30
152	LG:027320.7:2001MAR30	548	LG:027320.7.orf2:2001MAR30
153	LG:147541.44:2001MAR30	549	LG:147541.44.orf2:2001MAR30
154	LG:228319.2:2001MAR30	550	LG:228319.2.orf1:2001MAR30
155	LG:238754.19:2001MAR30	551	LG:238754.19.orf1:2001MAR30
156	LG:405751.12:2001MAR30	552	LG:405751.12.orf2:2001MAR30
157	U:011822.6:2001MAY17	553	U:011822.6.orf3:2001MAY17
158	U:1012467.2:2001MAY17	554	U:1012467.2.orf3:2001MAY17
159	U:1169981.13:2001MAY17	555	U:1169981.13.orf2:2001MAY17
160	U:1171553.1:2001MAY17	556	U:1171553.1.orf3:2001MAY17
161	U:1183156.3:2001MAY17	557	U:1183156.3.orf2:2001MAY17
162	U:1188500.6:2001MAY17	558	U:1188500.6.orf3:2001MAY17
163	U:147333.12:2001MAY17	559	U:147333.12.orf2:2001MAY17
164	U:147523.7:2001MAY17	560	U:147523.7.orf3:2001MAY17
165	U:197388.10:2001MAY17	561	U:197388.10.orf2:2001MAY17
166	U:2049216.1:2001MAY17	562	U:2049216.1.orf2:2001MAY17
167	U:2051624.2:2001MAY17	563	U:2051624.2.orf3:2001MAY17
168	U:2121838.1:2001MAY17	564	U:2121838.1.orf3:2001MAY17
169	U:2122954.8:2001MAY17	565	U:2122954.8.orf1:2001MAY17
170	U:2198064.2:2001MAY17	566	U:2198064.2.orf3:2001MAY17
171	U:2206583.1:2001MAY17	567	U:2206583.1.orf3:2001MAY17
172	U:235663.6:2001MAY17	568	U:235663.6.orf3:2001MAY17
173	U:236386.7:2001MAY17	569	U:236386.7.orf2:2001MAY17
174	U:236654.3:2001MAY17	570	U:236654.3.orf3:2001MAY17
175	U:256059.46:2001MAY17	571	U:256059.46.orf1:2001MAY17
176	U:279978.22:2001MAY17	572	U:279978.22.orf2:2001MAY17
177	U:311541.6:2001MAY17	573	U:311541.6.orf3:2001MAY17
178	U:346123.1:2001MAY17	574	U:346123.1.orf2:2001MAY17
179	U:381211.5:2001MAY17	575	U:381211.5.orf3:2001MAY17
180	U:412197.82:2001MAY17	576	U:412197.82.orf2:2001MAY17
181	U:412936.49:2001MAY17	577	U:412936.49.orf1:2001MAY17
182	U:427792.139:2001MAY17	578	U:427792.139.orf3:2001MAY17
183	U:450229.1:2001MAY17	579	U:450229.1.orf1:2001MAY17
184	U:475565.243:2001MAY17	580	U:475565.243.orf3:2001MAY17
185	U:764701.8:2001MAY17	581	U:764701.8.orf2:2001MAY17
186	U:024124.2:2001MAY17	582	U:024124.2.orf3:2001MAY17
187	U:038252.3:2001MAY17	583	U:038252.3.orf1:2001MAY17
188	U:056882.1:2001MAY17	584	U:056882.1.orf1:2001MAY17
189	U:059530.1:2001MAY17	585	U:059530.1.orf2:2001MAY17
190	U:089950.30:2001MAY17	586	U:089950.30.orf3:2001MAY17
191	U:1072906.38:2001MAY17	587	U:1072906.38.orf2:2001MAY17
192	U:1158936.4:2001MAY17	588	U:1158936.4.orf1:2001MAY17
193	U:1173412.15:2001MAY17	589	U:1173412.15.orf2:2001MAY17
194	U:1174279.14:2001MAY17	590	U:1174279.14.orf3:2001MAY17
195	U:1174809.1:2001MAY17	591	U:1174809.1.orf2:2001MAY17
196	U:1175131.1:2001MAY17	592	U:1175131.1.orf2:2001MAY17
197	U:1188801.10:2001MAY17	593	U:1188801.10.orf1:2001MAY17
198	U:1189176.27:2001MAY17	594	U:1189176.27.orf2:2001MAY17
199	U:197739.4:2001MAY17	595	U:197739.4.orf3:2001MAY17
200	U:2049016.1:2001MAY17	596	U:2049016.1.orf2:2001MAY17

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
201	U:2049137.1:2001MAY17	597	U:2049137.1.orf2:2001MAY17
202	U:2051907.1:2001MAY17	598	U:2051907.1.orf3:2001MAY17
203	U:2117996.13:2001MAY17	599	U:2117996.13.orf3:2001MAY17
204	U:2118683.15:2001MAY17	600	U:2118683.15.orf1:2001MAY17
205	U:2120312.1:2001MAY17	601	U:2120312.1.orf2:2001MAY17
206	U:2121328.17:2001MAY17	602	U:2121328.17.orf3:2001MAY17
207	U:2121802.5:2001MAY17	603	U:2121802.5.orf2:2001MAY17
208	U:2123406.9:2001MAY17	604	U:2123406.9.orf1:2001MAY17
209	U:216129.45:2001MAY17	605	U:216129.45.orf3:2001MAY17
210	U:2186630.1:2001MAY17	606	U:2186630.1.orf3:2001MAY17
211	U:2188206.2:2001MAY17	607	U:2188206.2.orf3:2001MAY17
212	U:2199710.9:2001MAY17	608	U:2199710.9.orf3:2001MAY17
213	U:2209335.2:2001MAY17	609	U:2209335.2.orf3:2001MAY17
214	U:230980.13:2001MAY17	610	U:230980.13.orf1:2001MAY17
215	U:244421.37:2001MAY17	611	U:244421.37.orf2:2001MAY17
216	U:341998.1:2001MAY17	612	U:341998.1.orf2:2001MAY17
217	U:347931.10:2001MAY17	613	U:347931.10.orf2:2001MAY17
218	U:350771.42:2001MAY17	614	U:350771.42.orf3:2001MAY17
219	U:354423.6:2001MAY17	615	U:354423.6.orf3:2001MAY17
220	U:399333.8:2001MAY17	616	U:399333.8.orf2:2001MAY17
221	U:445084.36:2001MAY17	617	U:445084.36.orf3:2001MAY17
222	U:454087.3:2001MAY17	618	U:454087.3.orf1:2001MAY17
223	U:474887.1:2001MAY17	619	U:474887.1.orf2:2001MAY17
224	U:745251.1:2001MAY17	620	U:745251.1.orf1:2001MAY17
225	U:747717.9:2001MAY17	621	U:747717.9.orf1:2001MAY17
226	U:806211.3:2001MAY17	622	U:806211.3.orf3:2001MAY17
227	U:815072.1:2001MAY17	623	U:815072.1.orf1:2001MAY17
228	U:817052.8:2001MAY17	624	U:817052.8.orf1:2001MAY17
229	U:903392.45:2001MAY17	625	U:903392.45.orf3:2001MAY17
230	U:013724.1:2001MAY17	626	U:013724.1.orf2:2001MAY17
231	U:191726.16:2001MAY17	627	U:191726.16.orf2:2001MAY17
232	U:202270.2:2001MAY17	628	U:202270.2.orf3:2001MAY17
233	U:2119352.6:2001MAY17	629	U:2119352.6.orf1:2001MAY17
234	U:2207776.11:2001MAY17	630	U:2207776.11.orf3:2001MAY17
235	U:256442.1:2001MAY17	631	U:256442.1.orf3:2001MAY17
236	U:330497.7:2001MAY17	632	U:330497.7.orf1:2001MAY17
237	U:018494.1:2001MAY17	633	U:018494.1.orf1:2001MAY17
238	U:023518.2:2001MAY17	634	U:023518.2.orf3:2001MAY17
239	U:053488.46:2001MAY17	635	U:053488.46.orf1:2001MAY17
240	U:058298.27:2001MAY17	636	U:058298.27.orf2:2001MAY17
241	U:1110046.1:2001MAY17	637	U:1110046.1.orf3:2001MAY17
242	U:1166752.11:2001MAY17	638	U:1166752.11.orf3:2001MAY17
243	U:1173766.1:2001MAY17	639	U:1173766.1.orf1:2001MAY17
244	U:1177952.4:2001MAY17	640	U:1177952.4.orf3:2001MAY17
245	U:1178064.3:2001MAY17	641	U:1178064.3.orf1:2001MAY17
246	U:1183121.1:2001MAY17	642	U:1183121.1.orf3:2001MAY17
247	U:1190431.13:2001MAY17	643	U:1190431.13.orf1:2001MAY17
248	U:199121.14:2001MAY17	644	U:199121.14.orf3:2001MAY17
249	U:202630.5:2001MAY17	645	U:202630.5.orf2:2001MAY17
250	U:2034488.1:2001MAY17	646	U:2034488.1.orf2:2001MAY17

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
251	U:2051434.8:2001MAY17	647	U:2051434.8.orf1:2001MAY17
252	U:2118475.9:2001MAY17	648	U:2118475.9.orf1:2001MAY17
253	U:218849.24:2001MAY17	649	U:218849.24.orf2:2001MAY17
254	U:2199824.5:2001MAY17	650	U:2199824.5.orf3:2001MAY17
255	U:233018.32:2001MAY17	651	U:233018.32.orf2:2001MAY17
256	U:236295.8:2001MAY17	652	U:236295.8.orf1:2001MAY17
257	U:286989.14:2001MAY17	653	U:286989.14.orf1:2001MAY17
258	U:345320.4:2001MAY17	654	U:345320.4.orf2:2001MAY17
259	U:355693.18:2001MAY17	655	U:355693.18.orf1:2001MAY17
260	U:359876.1:2001MAY17	656	U:359876.1.orf2:2001MAY17
261	U:406664.32:2001MAY17	657	U:406664.32.orf1:2001MAY17
262	U:410324.1:2001MAY17	658	U:410324.1.orf2:2001MAY17
263	U:414376.12:2001MAY17	659	U:414376.12.orf2:2001MAY17
264	U:452089.1:2001MAY17	660	U:452089.1.orf2:2001MAY17
265	U:481614.43:2001MAY17	661	U:481614.43.orf3:2001MAY17
266	U:809605.2:2001MAY17	662	U:809605.2.orf3:2001MAY17
267	U:816437.25:2001MAY17	663	U:816437.25.orf3:2001MAY17
268	U:817827.5:2001MAY17	664	U:817827.5.orf2:2001MAY17
269	U:002345.15:2001MAY17	665	U:002345.15.orf3:2001MAY17
270	U:022629.5:2001MAY17	666	U:022629.5.orf2:2001MAY17
271	U:061031.4:2001MAY17	667	U:061031.4.orf2:2001MAY17
272	U:108232.2:2001MAY17	668	U:108232.2.orf2:2001MAY17
273	U:1085493.16:2001MAY17	669	U:1085493.16.orf1:2001MAY17
274	U:1085513.2:2001MAY17	670	U:1085513.2.orf3:2001MAY17
275	U:1086797.9:2001MAY17	671	U:1086797.9.orf1:2001MAY17
276	U:1088446.1:2001MAY17	672	U:1088446.1.orf3:2001MAY17
277	U:1133764.3:2001MAY17	673	U:1133764.3.orf2:2001MAY17
278	U:1147614.5:2001MAY17	674	U:1147614.5.orf3:2001MAY17
279	U:1181710.1:2001MAY17	675	U:1181710.1.orf1:2001MAY17
280	U:1183192.1:2001MAY17	676	U:1183192.1.orf2:2001MAY17
281	U:1188786.15:2001MAY17	677	U:1188786.15.orf3:2001MAY17
282	U:145626.1:2001MAY17	678	U:145626.1.orf1:2001MAY17
283	U:147869.3:2001MAY17	679	U:147869.3.orf1:2001MAY17
284	U:151747.4:2001MAY17	680	U:151747.4.orf1:2001MAY17
285	U:198296.1:2001MAY17	681	U:198296.1.orf1:2001MAY17
286	U:200117.4:2001MAY17	682	U:200117.4.orf1:2001MAY17
287	U:200704.1:2001MAY17	683	U:200704.1.orf3:2001MAY17
288	U:2049995.3:2001MAY17	684	U:2049995.3.orf1:2001MAY17
289	U:2052097.2:2001MAY17	685	U:2052097.2.orf3:2001MAY17
290	U:209351.22:2001MAY17	686	U:209351.22.orf3:2001MAY17
291	U:2120481.1:2001MAY17	687	U:2120481.1.orf3:2001MAY17
292	U:2121610.13:2001MAY17	688	U:2121610.13.orf3:2001MAY17
293	U:2191585.1:2001MAY17	689	U:2191585.1.orf1:2001MAY17
294	U:2198562.3:2001MAY17	690	U:2198562.3.orf2:2001MAY17
295	U:2209684.5:2001MAY17	691	U:2209684.5.orf2:2001MAY17
296	U:222795.28:2001MAY17	692	U:222795.28.orf1:2001MAY17
297	U:228273.25:2001MAY17	693	U:228273.25.orf2:2001MAY17
298	U:232386.31:2001MAY17	694	U:232386.31.orf3:2001MAY17
299	U:233089.2:2001MAY17	695	U:233089.2.orf2:2001MAY17
300	U:240641.10:2001MAY17	696	U:240641.10.orf2:2001MAY17



TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
301	U:243871.4:2001MAY17	697	U:243871.4.orf2:2001MAY17
302	U:245597.7:2001MAY17	698	U:245597.7.orf2:2001MAY17
303	U:256009.31:2001MAY17	699	U:256009.31.orf1:2001MAY17
304	U:262221.1:2001MAY17	700	U:262221.1.orf3:2001MAY17
305	U:332957.8:2001MAY17	701	U:332957.8.orf3:2001MAY17
306	U:335352.13:2001MAY17	702	U:335352.13.orf2:2001MAY17
307	U:343844.7:2001MAY17	703	U:343844.7.orf3:2001MAY17
308	U:344528.1:2001MAY17	704	U:344528.1.orf1:2001MAY17
309	U:374578.27:2001MAY17	705	U:374578.27.orf1:2001MAY17
310	U:381993.13:2001MAY17	706	U:381993.13.orf3:2001MAY17
311	U:400373.2:2001MAY17	707	U:400373.2.orf1:2001MAY17
312	U:400963.6:2001MAY17	708	U:400963.6.orf3:2001MAY17
313	U:404874.8:2001MAY17	709	U:404874.8.orf2:2001MAY17
314	U:405158.18:2001MAY17	710	U:405158.18.orf2:2001MAY17
315	U:405889.22:2001MAY17	711	U:405889.22.orf2:2001MAY17
316	U:411151.31:2001MAY17	712	U:411151.31.orf1:2001MAY17
317	U:411313.51:2001MAY17	713	U:411313.51.orf2:2001MAY17
318	U:417127.1:2001MAY17	714	U:417127.1.orf1:2001MAY17
319	U:429817.44:2001MAY17	715	U:429817.44.orf3:2001MAY17
320	U:474134.23:2001MAY17	716	U:474134.23.orf3:2001MAY17
321	U:475378.3:2001MAY17	717	U:475378.3.orf2:2001MAY17
322	U:749588.15:2001MAY17	718	U:749588.15.orf3:2001MAY17
323	U:757736.17:2001MAY17	719	U:757736.17.orf1:2001MAY17
324	U:817278.4:2001MAY17	720	U:817278.4.orf2:2001MAY17
325	U:027320.5:2001MAY17	721	U:027320.5.orf2:2001MAY17
326	U:204635.5:2001MAY17	722	U:204635.5.orf2:2001MAY17
327	U:215532.38:2001MAY17	723	U:215532.38.orf2:2001MAY17
328	U:228319.6:2001MAY17	724	U:228319.6.orf2:2001MAY17
329	U:236589.24:2001MAY17	725	U:236589.24.orf2:2001MAY17
330	U:247444.3:2001MAY17	726	U:247444.3.orf2:2001MAY17
331	U:332404.20:2001MAY17	727	U:332404.20.orf3:2001MAY17
332	LG:1088459.4:2001JUN22	728	LG:1088459.4.orf2:2001JUN22
333	LG:1501495.1:2001JUN22	729	LG:1501495.1.orf1:2001JUN22
334	LG:334284.10:2001JUN22	730	LG:334284.10.orf1:2001JUN22
335	LG:345279.19:2001JUN22	731	LG:345279.19.orf1:2001JUN22
336	LG:7689681.1:2001JUN22	732	LG:7689681.1.orf1:2001JUN22
337	LG:7690093.1:2001JUN22	733	LG:7690093.1.orf3:2001JUN22
338	LG:7690175.3:2001JUN22	734	LG:7690175.3.orf2:2001JUN22
339	LG:7697128.1:2001JUN22	735	LG:7697128.1.orf2:2001JUN22
340	LG:006394.20:2001JUN22	736	LG:006394.20.orf1:2001JUN22
341	LG:1012069.1:2001JUN22	737	LG:1012069.1.orf1:2001JUN22
342	LG:104533.11:2001JUN22	738	LG:104533.11.orf2:2001JUN22
343	LG:1045853.23:2001JUN22	739	LG:1045853.23.orf1:2001JUN22
344	LG:1081017.8:2001JUN22	740	LG:1081017.8.orf3:2001JUN22
345	LG:1090358.6:2001JUN22	741	LG:1090358.6.orf3:2001JUN22
346	LG:1135312.7:2001JUN22	742	LG:1135312.7.orf2:2001JUN22
347	LG:1328501.2:2001JUN22	743	LG:1328501.2.orf1:2001JUN22
348	LG:133095.1:2001JUN22	744	LG:133095.1.orf3:2001JUN22
349	LG:135379.5:2001JUN22	745	LG:135379.5.orf1:2001JUN22
350	LG:1365581.3:2001JUN22	746	LG:1365581.3.orf1:2001JUN22

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
351	LG:1383156.20:2001JUN22	747	LG:1383156.20.orf2:2001JUN22
352	LG:1501767.18:2001JUN22	748	LG:1501767.18.orf3:2001JUN22
353	LG:1501890.8:2001JUN22	749	LG:1501890.8.orf1:2001JUN22
354	LG:203434.23:2001JUN22	750	LG:203434.23.orf2:2001JUN22
355	LG:204724.5:2001JUN22	751	LG:204724.5.orf3:2001JUN22
356	LG:257107.16:2001JUN22	752	LG:257107.16.orf3:2001JUN22
357	LG:353530.4:2001JUN22	753	LG:353530.4.orf1:2001JUN22
358	LG:7683573.3:2001JUN22	754	LG:7683573.3.orf1:2001JUN22
359	LG:7684224.1:2001JUN22	755	LG:7684224.1.orf1:2001JUN22
360	LG:7690365.2:2001JUN22	756	LG:7690365.2.orf3:2001JUN22
361	LG:968691.1:2001JUN22	757	LG:968691.1.orf1:2001JUN22
362	LG:983076.7:2001JUN22	758	LG:983076.7.orf2:2001JUN22
363	LG:986291.1:2001JUN22	759	LG:986291.1.orf1:2001JUN22
364	LG:990347.41:2001JUN22	760	LG:990347.41.orf3:2001JUN22
365	LG:998305.4:2001JUN22	761	LG:998305.4.orf3:2001JUN22
366	LG:463420.16:2001JUN22	762	LG:463420.16.orf1:2001JUN22
367	LG:979059.3:2001JUN22	763	LG:979059.3.orf1:2001JUN22
368	LG:1045509.22:2001JUN22	764	LG:1045509.22.orf2:2001JUN22
369	LG:246935.4:2001JUN22	765	LG:246935.4.orf1:2001JUN22
370	LG:321069.2:2001JUN22	766	LG:321069.2.orf1:2001JUN22
371	LG:346724.14:2001JUN22	767	LG:346724.14.orf1:2001JUN22
372	LG:411043.3:2001JUN22	768	LG:411043.3.orf2:2001JUN22
373	LG:978620.7:2001JUN22	769	LG:978620.7.orf3:2001JUN22
374	LG:982784.1:2001JUN22	770	LG:982784.1.orf3:2001JUN22
375	LG:007574.21:2001JUN22	771	LG:007574.21.orf1:2001JUN22
376	LG:013856.18:2001JUN22	772	LG:013856.18.orf2:2001JUN22
377	LG:027320.7:2001JUN22	773	LG:027320.7.orf2:2001JUN22
378	LG:077967.9:2001JUN22	774	LG:077967.9.orf1:2001JUN22
379	LG:128475.9:2001JUN22	775	LG:128475.9.orf2:2001JUN22
380	LG:1398104.15:2001JUN22	776	LG:1398104.15.orf3:2001JUN22
381	LG:1454018.10:2001JUN22	777	LG:1454018.10.orf3:2001JUN22
382	LG:221548.14:2001JUN22	778	LG:221548.14.orf2:2001JUN22
383	LG:227500.5:2001JUN22	779	LG:227500.5.orf2:2001JUN22
384	LG:228273.22:2001JUN22	780	LG:228273.22.orf2:2001JUN22
385	LG:235432.1:2001JUN22	781	LG:235432.1.orf1:2001JUN22
386	LG:236904.20:2001JUN22	782	LG:236904.20.orf3:2001JUN22
387	LG:253193.21:2001JUN22	783	LG:253193.21.orf2:2001JUN22
388	LG:332161.3:2001JUN22	784	LG:332161.3.orf2:2001JUN22
389	LG:332923.5:2001JUN22	785	LG:332923.5.orf2:2001JUN22
390	LG:343500.27:2001JUN22	786	LG:343500.27.orf3:2001JUN22
391	LG:369703.9:2001JUN22	787	LG:369703.9.orf1:2001JUN22
392	LG:415378.3:2001JUN22	788	LG:415378.3.orf1:2001JUN22
393	LG:458583.1:2001JUN22	789	LG:458583.1.orf1:2001JUN22
394	LG:7690373.1:2001JUN22	790	LG:7690373.1.orf1:2001JUN22
395	LG:898324.13:2001JUN22	791	LG:898324.13.orf1:2001JUN22
396	LG:979167.5:2001JUN22	792	LG:979167.5.orf3:2001JUN22

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
1	LG:036272.1:2001MAR30	g12846107	1.00E-112	putative (Mus musculus)
2	LG:093337.3:2001MAR30	g12652727	2.00E-31	Unknown (protein for IMAGE:3352566) (Homo sapiens)
3	LG:1049927.6:2001MAR30	g16551755	6.00E-49	unnamed protein product (Homo sapiens)
4	LG:1051891.34:2001MAR30	g38032	0	ZNF43 (Homo sapiens)
5	LG:1089626.1:2001MAR30	g16549180	0	unnamed protein product (Homo sapiens)
6	LG:1101416.6:2001MAR30	g872315	4.00E-47	40S ribosomal protein S12 (Sus scrofa)
7	LG:1295974.1:2001MAR30	g485373	1.00E-104	ferritin heavy chain (Mus musculus)
8	LG:1400572.2:2001MAR30	g12052983	2.00E-62	hypothetical protein (Homo sapiens)
9	LG:1446621.1:2001MAR30	g7959207	2.00E-38	KIAA1473 protein (Homo sapiens)
10	LG:1499752.1:2001MAR30	g339697	2.00E-18	thymosin beta-10 (Homo sapiens)
11	LG:1503044.7:2001MAR30	g15929821	1.00E-117	putative Rab5 GDP/GTP exchange factor homologue (Homo sapiens)
12	LG:1503588.1:2001MAR30	g7959207	1.00E-38	KIAA1473 protein (Homo sapiens)
13	LG:1503589.2:2001MAR30	g16552245	1.00E-162	unnamed protein product (Homo sapiens)
14	LG:1506339.4:2001MAR30	g17512041	1.00E-124	Unknown (protein for MGC:20302) (Homo sapiens)
15	LG:220648.6:2001MAR30	g12310941	2.00E-60	unnamed protein product (Homo sapiens)
16	LG:236654.1:2001MAR30	g12843135	1.00E-135	putative (Mus musculus)
17	LG:237699.26:2001MAR30	g388168	1.00E-127	Bax beta (Homo sapiens)
18	LG:311541.16:2001MAR30	g15209690	0	unnamed protein product (Homo sapiens)
19	LG:335923.7:2001MAR30	g15717944	4.00E-76	ba14C22.1 (novel protein similar to lysozyme) (Homo sapiens)
20	LG:350342.14:2001MAR30	g15079361	3.00E-94	Similar to PCTAIRE-motif protein kinase 3 (Homo sapiens)
21	LG:369301.32:2001MAR30	g14149068	0	hypothetical protein (Homo sapiens)
22	LG:452089.1:2001MAR30	g7340874	5.00E-88	ESTs D15590(C0900),D48950(S15542),D22684(C0900) correspond to a region of the predicted gene. ~Similar to Arabidopsis thaliana 60S ribosomal protein L11A (L16A). (P42795) (Oryza sativa)
23	LG:454087.3:2001MAR30	g2689446	0	R27945_1 (Homo sapiens)
24	LG:466302.1:2001MAR30	g12847061	5.00E-97	putative (Mus musculus)
25	LG:474267.1:2001MAR30	g15487218	6.00E-17	MORN-domain protein (Leishmania major)
26	LG:995613.10:2001MAR30	g6807718	1.00E-128	hypothetical protein (Homo sapiens)
27	LG:011843.5:2001MAR30	g10998440	0	EGF-related protein SCUBE1 (Mus musculus)
28	LG:075904.32:2001MAR30	g12005908	1.00E-146	AD037 (Homo sapiens)
29	LG:1004781.3:2001MAR30	g14794726	0	CUB and sushi multiple domains 1 protein (Homo sapiens)

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
30	LG:1041807.8:2001MAR30	g2477513	0	F25965_3 (Homo sapiens)
31	LG:1044448.2:2001MAR30	g14307916	0	myosin phosphatase targeting subunit 3 MYPT3 (Mus musculus)
32	LG:1080598.9:2001MAR30	g7019945	1.00E-179	unnamed protein product (Homo sapiens)
33	LG:1081017.1:2001MAR30	g340080	7.00E-34	UDP-glucuronosyltransferase (EC 2.4.1.17) (Homo sapiens)
34	LG:1083120.2:2001MAR30	g14348588	5.00E-69	KRAB zinc finger protein (Homo sapiens)
35	LG:1097492.12:2001MAR30	g2224529	0	KIAA0294 (Homo sapiens)
36	LG:118834.9:2001MAR30	g7301264	1.00E-89	CG9996 gene product (Drosophila melanogaster)
37	LG:1227408.25:2001MAR30	g13121981	3.00E-90	unnamed protein product (Homo sapiens)
38	LG:1326953.1:2001MAR30	g190814	3.00E-40	Wilm's tumor-related protein (Homo sapiens)
39	LG:1397821.17:2001MAR30	g12847582	0	putative (Mus musculus)
40	LG:1512507.1:2001MAR30	g12832255	3.00E-79	putative (Mus musculus)
41	LG:196583.5:2001MAR30	g17483854	0	a disintegrin-like and metalloprotease with thrombospondin type 1 motif 14 precursor (Homo sapiens)
42	LG:198669.1:2001MAR30	g4160198	1.00E-120	dj327J16.3 (supported by GENSCAN, FGENES and GENEWISE) (Homo sapiens)
43	LG:202943.1:2001MAR30	g11177164	0	polydom protein (Mus musculus)
44	LG:204724.3:2001MAR30	g58491	0	E1b 55k protein (transformation) (Human adenovirus type 5)
45	LG:206425.10:2001MAR30	g1174187	0	purine nucleotide binding protein (Mus musculus)
46	LG:208190.2:2001MAR30	g15559603	0	Unknown (protein for MGC:20847) (Homo sapiens)
47	LG:222927.2:2001MAR30	g12836052	0	putative (Mus musculus)
48	LG:228046.5:2001MAR30	g3413918	0	KIAA0478 protein (Homo sapiens)
49	LG:230980.1:2001MAR30	g12842288	0	putative (Mus musculus)
50	LG:236976.2:2001MAR30	g3900848	3.00E-81	match to EST AA361117 (NID:g2013436) (Homo sapiens)
51	LG:238322.6:2001MAR30	g12081909	0	semaphorin Y (Homo sapiens)
52	LG:341461.1:2001MAR30	g14334177	1.00E-119	beta cysteine string protein (Homo sapiens)
53	LG:354088.1:2001MAR30	g7959193	2.00E-70	KIAA1466 protein (Homo sapiens)
54	LG:376275.1:2001MAR30	g6249687	6.00E-59	R31155_1 (Homo sapiens)
55	LG:399281.3:2001MAR30	g6634025	1.00E-151	KIAA0379 protein (Homo sapiens)
56	LG:404921.10:2001MAR30	g16741323	0	Similar to hypothetical protein DKFZp434L0718 (Mus musculus)
57	LG:444677.34:2001MAR30	g14424793	2.00E-59	Unknown (protein for MGC:15165) (Homo sapiens)
58	LG:968691.1:2001MAR30	g17105197	1.00E-108	kelch-like protein KLHL6 (Homo sapiens)

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
59	LG:983862.1:2001MAR30	g14274810	0	unnamed protein product (Homo sapiens)
60	LG:984130.1:2001MAR30	g10434090	0	unnamed protein product (Homo sapiens)
61	LG:986291.1:2001MAR30	g206734	1.00E-165	ribosomal protein L5 (Rattus norvegicus)
62	LG:045210.8:2001MAR30	g2827474	5.00E-87	predicted protein dJ257A7.2 (Homo sapiens)
63	LG:229284.39:2001MAR30	g5419859	0	hypothetical protein (Homo sapiens)
64	LG:337810.20:2001MAR30	g4106984	1.00E-120	R30923_1 (Homo sapiens)
65	LG:463420.1:2001MAR30	g7959265	0	KIAA1502 protein (Homo sapiens)
66	LG:1080918.1:2001MAR30	g16549907	0	unnamed protein product (Homo sapiens)
67	LG:1093747.15:2001MAR30	g13436440	0	Unknown (protein for MGC:4400) (Homo sapiens)
68	LG:1096896.47:2001MAR30	g12655061	1.00E-89	succinate dehydrogenase complex, subunit A, flavoprotein (Fp) (Homo sapiens)
69	LG:1098931.39:2001MAR30	g452316	0	acetyl-CoA carboxylase (Homo sapiens)
70	LG:1100823.1:2001MAR30	g5410605	5.00E-57	tetraspanin membrane protein CD63 (Mus musculus)
71	LG:1166387.1:2001MAR30	g7159799	0	dJ351K20.1.1 (novel C3HC4 type Zinc finger (RING finger) protein (isoform 1)) (Homo sapiens)
72	LG:1383036.49:2001MAR30	g2966650	1.00E-157	hnmp a1 protein (Homo sapiens)
73	LG:1452353.14:2001MAR30	g309453	0	neurofibromin (Mus musculus)
74	LG:1452435.15:2001MAR30	g178646	0	ankyrin (Homo sapiens)
75	LG:1498774.1:2001MAR30	g2668738	3.00E-89	translation initiation factor 5A (Zea mays)
76	LG:197180.1:2001MAR30	g556301	0	elongation factor Tu (Mus musculus)
77	LG:199489.1:2001MAR30	g476725	0	T-cell early activation protein (Mus musculus)
78	LG:201908.3:2001MAR30	g17391340	0	Unknown (protein for MGC:20009) (Homo sapiens)
79	LG:247245.26:2001MAR30	g16551429	1.00E-161	unnamed protein product (Homo sapiens)
80	LG:256365.2:2001MAR30	g15929959	1.00E-105	Similar to tropomyosin 4 (Homo sapiens)
81	LG:332923.4:2001MAR30	g13874450	0	hypothetical protein (Macaca fascicularis)
82	LG:335276.1:2001MAR30	g1477588	1.00E-140	DLX-1 (Mus musculus)
83	LG:350272.2:2001MAR30	g12845866	1.00E-72	putative (Mus musculus)
84	LG:350921.2:2001MAR30	g16508652	0	unnamed protein product (Homo sapiens)
85	LG:406568.1:2001MAR30	g12656196	1.00E-122	cardiac telomodin (Mus musculus)
86	LG:411043.3:2001MAR30	g12861800	0	putative (Mus musculus)
87	LG:414376.20:2001MAR30	g57667	0	put. RCK2 protein (AA 1-530) (Rattus rattus)
88	LG:457695.1:2001MAR30	g15810196	1.00E-111	AT3g13580/K20M4_2 (Arabidopsis thaliana)

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
89	LG:902390.2:2001MAR30	g12860912	4.00E-36	putative (Mus musculus)
90	LG:903565.20:2001MAR30	g769701	0	PACE4A (Mus musculus)
91	LG:978182.4:2001MAR30	g9651646	0	MRE11 (Rattus norvegicus)
92	LG:986827.1:2001MAR30	g12855841	1.00E-75	putative (Mus musculus)
93	LG:013792.1:2001MAR30	g15021881	5.00E-09	hypothetical protein (Macaca fascicularis)
94	LG:018258.1:2001MAR30	g12832288	1.00E-111	putative (Mus musculus)
95	LG:023126.3:2001MAR30	g2276313	2.00E-19	match: multiple proteins; match: Q08151 P28185 Q01111 Q43554; match: Q08150 Q40195 P20340 Q39222; match: Q40368 P36412 P40393 Q40723; match: CE01798 Q38923 Q40191 Q41022; match: Q39433 Q40177 Q40218 Q08146; match: P10949 P11023 Q16948 Q20337; match: Q25389 P25228 P20336 P05713; match: P35276 Q08147 P17609 P22128; match: Q15771 P36410 P35291; GTP-binding (Homo sapiens)
96	LG:023618.1:2001MAR30	g854065	2.00E-25	U88 (Human herpesvirus 6)
97	LG:030999.1:2001MAR30	g7271471	1.00E-158	Rab-related GTP-binding protein RabJ (Homo sapiens)
98	LG:103508.1:2001MAR30	g14597533	1.00E-171	unnamed protein product (Homo sapiens)
99	LG:107976.15:2001MAR30	g17128217	0	unnamed protein product (Homo sapiens)
100	LG:1080096.1:2001MAR30	g5080758	0	BC331191_1 (Homo sapiens)
101	LG:1080275.1:2001MAR30	g5262557	1.00E-88	hypothetical protein (Homo sapiens)
102	LG:1090358.10:2001MAR30	g3540177	1.00E-108	F23269_2 (Homo sapiens)
103	LG:1095833.9:2001MAR30	g4240143	0	KIAA0827 protein (Homo sapiens)
104	LG:1383121.25:2001MAR30	g7582292	3.00E-60	BM-010 (Homo sapiens)
105	LG:1386609.2:2001MAR30	g6330433	0	KIAA1203 protein (Homo sapiens)
106	LG:1398465.1:2001MAR30	g5410334	1.00E-128	WSB-1 isoform (Homo sapiens)
107	LG:1453417.10:2001MAR30	g9828190	0	FLAMINGO 1 (Homo sapiens)
108	LG:147869.3:2001MAR30	g16549477	0	unnamed protein product (Homo sapiens)
109	LG:148485.5:2001MAR30	g16768654	5.00E-45	HL01494p (Drosophila melanogaster)
110	LG:1501818.12:2001MAR30	g13182779	0	HCOBP (Homo sapiens)
111	LG:1508275.1:2001MAR30	g57175	6.00E-48	S-100 protein (Rattus norvegicus)
112	LG:1509771.1:2001MAR30	g12804565	4.00E-41	Unknown (protein for IMAGE:2989556) (Homo sapiens)
113	LG:1512998.13:2001MAR30	g15625568	1.00E-166	Run- and FYVE-domain containing protein Rabjp4R (Homo sapiens)
114	LG:198251.7:2001MAR30	g11493516	6.00E-34	PRO1107 (Homo sapiens)

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
115	LG:198296.1:2001MAR30	g7019911	0	unnamed protein product (Homo sapiens)
116	LG:198876.13:2001MAR30	g13359199	0	KIAA1663 protein (Homo sapiens)
117	LG:200704.1:2001MAR30	g9651089	1.00E-166	hypothetical protein (Macaca fascicularis)
118	LG:206593.3:2001MAR30	g12052983	1.00E-110	hypothetical protein (Homo sapiens)
119	LG:223970.11:2001MAR30	g4514554	0	Rod1 (Homo sapiens)
120	LG:227500.5:2001MAR30	g16356673	0	UM protein prickly b (Xenopus laevis)
121	LG:227722.7:2001MAR30	g3128218	1.00E-52	putative katanin (Arabidopsis thaliana)
122	LG:229105.1:2001MAR30	g16554016	0	unnamed protein product (Homo sapiens)
123	LG:233761.4:2001MAR30	g12407377	0	tripartite motif protein TRIM4 isoform alpha (Homo sapiens)
124	LG:234326.67:2001MAR30	g11610575	0	RTN-XL (Homo sapiens)
125	LG:236056.27:2001MAR30	g13543110	0	Similar to SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2 (Mus musculus)
126	LG:253889.31:2001MAR30	g189310	1.00E-163	nucleolysin TIAR (Homo sapiens)
127	LG:270833.135:2001MAR30	g12844788	4.00E-67	putative (Mus musculus)
128	LG:292613.7:2001MAR30	g10241461	1.00E-107	dJ1121G12.1.2 (A novel protein containing a putative PHD finger domain, isoform 2) (Homo sapiens)
129	LG:331546.2:2001MAR30	g1401126	0	TAK1 binding protein (Homo sapiens)
130	LG:332027.6:2001MAR30	g12832845	1.00E-162	putative (Mus musculus)
131	LG:336998.1:2001MAR30	g347377	0	MILL-AF4 der(11) fusion protein (Homo sapiens)
132	LG:338010.8:2001MAR30	g12860837	1.00E-163	putative (Mus musculus)
133	LG:344597.1:2001MAR30	g13603398	0	SEZ6L (Homo sapiens)
134	LG:347361.2:2001MAR30	g2914017	0	Ankhn (Mus musculus)
135	LG:349293.17:2001MAR30	g7239366	0	groucho-related protein 4 (Mus musculus)
136	LG:410595.19:2001MAR30	g13960126	1.00E-124	Similar to leucine-rich neuronal protein (Homo sapiens)
137	LG:411151.35:2001MAR30	g6969629	0	oracle.1 protein (Mus musculus)
138	LG:411334.8:2001MAR30	g1537017	0	UM protein (Homo sapiens)
139	LG:458583.1:2001MAR30	g7020724	6.00E-76	unnamed protein product (Homo sapiens)
140	LG:475378.1:2001MAR30	g7243105	1.00E-118	KIAA1362 protein (Homo sapiens)
141	LG:481572.1:2001MAR30	g6331213	0	KIAA1268 protein (Homo sapiens)
142	LG:481704.1:2001MAR30	g7959193	2.00E-81	KIAA1466 protein (Homo sapiens)
143	LG:898195.4:2001MAR30	g7243777	0	Diablo (Drosophila melanogaster)

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
144	LG:903785.1:2001MAR30	g7242951	0	KIAA1298 protein (Homo sapiens)
145	LG:977454.3:2001MAR30	g12844142	2.00E-68	putative (Mus musculus)
146	LG:977724.12:2001MAR30	g10432612	0	unnamed protein product (Homo sapiens)
147	LG:978215.19:2001MAR30	g9309467	1.00E-136	leucine-rich glioma-inactivated 1 protein precursor (Mus musculus)
148	LG:981795.1:2001MAR30	g5410527	1.00E-150	paracellin-1 (Homo sapiens)
149	LG:982784.1:2001MAR30	g16553391	1.00E-136	unnamed protein product (Homo sapiens)
150	LG:987322.4:2001MAR30	g11596121	0	SIR2alpha protein (Homo sapiens)
151	LG:006242.7:2001MAR30	g9997097	0	unnamed protein product (Homo sapiens)
152	LG:027320.7:2001MAR30	g16553765	0	unnamed protein product (Homo sapiens)
153	LG:147541.44:2001MAR30	g14318590	1.00E-103	Unknown (protein for MGC:7100) (Mus musculus)
154	LG:228319.2:2001MAR30	g16041142	1.00E-133	hypothetical protein (Macaca fascicularis)
155	LG:238754.19:2001MAR30	g13477109	1.00E-67	RIKEN cDNA 0610043B10 gene (Homo sapiens)
156	LG:405751.12:2001MAR30	g1711238	0	TIS (Mus musculus)
157	LI:011822.6:2001MAY17	g16359265	6.00E-87	Similar to hypothetical protein DKFp434G2226 (Mus musculus)
158	LI:1012467.2:2001MAY17	g16550592	1.00E-169	unnamed protein product (Homo sapiens)
159	LI:1169981.13:2001MAY17	g4235144	1.00E-158	BC39498_1 (Homo sapiens)
160	LI:1171553.1:2001MAY17	g16549180	0	unnamed protein product (Homo sapiens)
161	LI:1183156.3:2001MAY17	g4164083	0	zinc finger protein EZNF (Homo sapiens)
162	LI:1188500.6:2001MAY17	g16508614	0	unnamed protein product (Homo sapiens)
163	LI:147333.12:2001MAY17	g12654987	1.00E-60	Unknown (protein for MGC:5621) (Homo sapiens)
164	LI:147523.7:2001MAY17	g6018682	2.00E-85	superoxide dismutase-4AP (Zea mays)
165	LI:197388.10:2001MAY17	g13279311	1.00E-165	Similar to RIKEN cDNA 1500017E18 gene (Homo sapiens)
166	LI:2049216.1:2001MAY17	g15866260	1.00E-148	MRIP2 (Homo sapiens)
167	LI:2051624.2:2001MAY17	g14602654	0	Unknown (protein for MGC:15400) (Homo sapiens)
168	LI:2121838.1:2001MAY17	g16552172	1.00E-114	unnamed protein product (Homo sapiens)
169	LI:2122954.8:2001MAY17	g10435738	1.00E-124	unnamed protein product (Homo sapiens)
170	LI:2198064.2:2001MAY17	g12652727	3.00E-29	Unknown (protein for IMAGE:3352566) (Homo sapiens)
171	LI:2206583.1:2001MAY17	g16553223	1.00E-106	unnamed protein product (Homo sapiens)
172	LI:2356663.6:2001MAY17	g16973457	6.00E-56	beta-3-galactosyltransferase (Danio rerio)
173	LI:236386.7:2001MAY17	g17511850	0	Unknown (protein for MGC:32065) (Homo sapiens)
174	LI:236654.3:2001MAY17	g11602755	1.00E-133	zinc finger protein (Mus musculus)



Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
175	LI:256059.46:2001MAY17	g9971114	1.00E-115	MHC class I antigen (Homo sapiens)
176	LI:279978.22:2001MAY17	g13517077	0	lipote-activating enzyme (Bos taurus)
177	LI:311541.6:2001MAY17	g15209690	0	unnamed protein product (Homo sapiens)
178	LI:346123.1:2001MAY17	g168647	1.00E-143	fructosephosphate isomerase 1 (Zea mays)
179	LI:381211.5:2001MAY17	g13160045	0	dJ734P14.5 (novel C2H2 type zinc finger protein) (Homo sapiens)
180	LI:412197.82:2001MAY17	g17512041	3.00E-71	Unknown (protein for MGC:20302) (Homo sapiens)
181	LI:412936.49:2001MAY17	g10801585	1.00E-109	PQBP-1b/c (Homo sapiens)
182	LI:427792.139:2001MAY17	g1811178	2.00E-61	lysosomal proteinase cathepsin B (Homo sapiens)
183	LI:450229.1:2001MAY17	g4588906	1.00E-96	ribosomal protein S7 (Secale cereale)
184	LI:475565.243:2001MAY17	g16553223	4.00E-99	unnamed protein product (Homo sapiens)
185	LI:764701.8:2001MAY17	g12841311	8.00E-90	putative (Mus musculus)
186	LI:024124.2:2001MAY17	g11094295	0	brain link protein-1 (Mus musculus)
187	LI:038252.3:2001MAY17	g4186185	0	unknown (Homo sapiens)
188	LI:056882.1:2001MAY17	g6249687	3.00E-59	R31155_1 (Homo sapiens)
189	LI:059530.1:2001MAY17	g232783	7.00E-33	Purkinje cell protein 2; Pcp-2 (Mus sp.)
190	LI:089950.30:2001MAY17	g14042915	0	unnamed protein product (Homo sapiens)
191	LI:1072906.38:2001MAY17	g13279044	0	hypothetical protein PRO1741 (Homo sapiens)
192	LI:1158936.4:2001MAY17	g13274611	1.00E-169	glutamate rich WD repeat protein (Homo sapiens)
193	LI:1173412.15:2001MAY17	g14602971	0	Unknown (protein for MGC:14981) (Homo sapiens)
194	LI:1174279.14:2001MAY17	g3540177	0	F23269_2 (Homo sapiens)
195	LI:1174809.1:2001MAY17	g7959207	1.00E-126	KIAA1473 protein (Homo sapiens)
196	LI:1175131.1:2001MAY17	g6467202	0	gonadotropin inducible transcription repressor-2 (Homo sapiens)
197	LI:1188801.10:2001MAY17	g5231271	0	autoimmune enteropathy-related antigen AIE-75 (Homo sapiens)
198	LI:1189176.27:2001MAY17	g15823640	4.00E-79	Als2 (Mus musculus)
199	LI:197739.4:2001MAY17	g3417297	0	Unknown gene product (Homo sapiens)
200	LI:2049016.1:2001MAY17	g16550359	3.00E-39	unnamed protein product (Homo sapiens)
201	LI:2049137.1:2001MAY17	g13937909	1.00E-108	Similar to KIAA0961 protein (Homo sapiens)
202	LI:2051907.1:2001MAY17	g16549529	0	unnamed protein product (Homo sapiens)
203	LI:2117996.13:2001MAY17	g3256185	1.00E-121	dJ510H16.1 (target of myb1 (chicken) homolog) (Homo sapiens)
204	LI:2118683.15:2001MAY17	g13676443	1.00E-116	hypothetical protein (Macaca fascicularis)
205	LI:2120312.1:2001MAY17	g15213812	2.00E-38	ribosomal protein S12 (Spodoptera frugiperda)

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
206	U:2121328.17:2001MAY17	g12314195	8.00E-74	bA255A11.3 (novel protein similar to KIAA1074) (Homo sapiens)
207	U:2121802.5:2001MAY17	g16550359	0	unnamed protein product (Homo sapiens)
208	U:2123406.9:2001MAY17	g15620839	9.00E-95	KIAA1890 protein (Homo sapiens)
209	U:21216129.45:2001MAY17	g13160494	0	UBX domain-containing protein 1 (Homo sapiens)
210	U:2186630.1:2001MAY17	g16549907	4.00E-41	unnamed protein product (Homo sapiens)
211	U:2188206.2:2001MAY17	g4185943	1.00E-73	pol protein (Human endogenous retrovirus K)
212	U:2199710.9:2001MAY17	g499204	1.00E-84	D-E-A-D box protein (Drosophila melanogaster)
213	U:2209335.2:2001MAY17	g12314164	1.00E-150	bA526D8.2 (novel protein similar to KIAA1074) (Homo sapiens)
214	U:230980.13:2001MAY17	g12842288	1.00E-166	putative (Mus musculus)
215	U:244421.37:2001MAY17	g7188556	1.00E-104	CpG binding protein (Homo sapiens)
216	U:341998.1:2001MAY17	g17016967	3.00E-67	NUANCE (Homo sapiens)
217	U:347931.10:2001MAY17	g6634023	0	KIAA0356 protein (Homo sapiens)
218	U:350771.42:2001MAY17	g15963476	1.00E-103	alpha-adaptin A related protein (Homo sapiens)
219	U:354423.6:2001MAY17	g14042035	0	unnamed protein product (Homo sapiens)
220	U:399333.8:2001MAY17	g15559519	0	Unknown (protein for IMAGE:4561365) (Homo sapiens)
221	U:445084.36:2001MAY17	g12840887	3.00E-55	putative (Mus musculus)
222	U:454087.3:2001MAY17	g2689446	0	R27945_1 (Homo sapiens)
223	U:474887.1:2001MAY17	g2597931	1.00E-42	ubiquitin-conjugating enzyme, UBC9 (Homo sapiens)
224	U:745251.1:2001MAY17	g17105197	1.00E-174	kelch-like protein KLHL6 (Homo sapiens)
225	U:747717.9:2001MAY17	g11544425	0	bG153O3.1 (similar to C.elegans hemikenttin precursor) (Homo sapiens)
226	U:806211.3:2001MAY17	g7019945	1.00E-119	unnamed protein product (Homo sapiens)
227	U:815072.1:2001MAY17	g402827	3.00E-40	QM (Homo sapiens)
228	U:817052.8:2001MAY17	g6331377	0	KIAA1285 protein (Homo sapiens)
229	U:903392.45:2001MAY17	g15072406	1.00E-147	TNFAIP1-like protein (Homo sapiens)
230	U:013724.1:2001MAY17	g13277864	1.00E-161	Similar to ATPase, H+ transporting, lysosomal (vacuolar proton pump) 42kD (Mus musculus)
231	U:191726.16:2001MAY17	g1208742	0	protein B (Homo sapiens)
232	U:202270.2:2001MAY17	g16549383	4.00E-74	unnamed protein product (Homo sapiens)
233	U:2119352.6:2001MAY17	g14043223	2.00E-95	Unknown (protein for MGC:15677) (Homo sapiens)
234	U:2207776.11:2001MAY17	g7294748	9.00E-99	CG7616 gene product (Drosophila melanogaster)
235	U:256442.1:2001MAY17	g16265875	4.00E-51	proline-rich acidic protein (Homo sapiens)

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
236	U:330497.7:2001MAY17	g17064172	1.00E-80	NALP4 (Homo sapiens)
237	U:018494.1:2001MAY17	g17389275	0	Unknown (protein for MGC:19357) (Mus musculus)
238	U:023518.2:2001MAY17	g3955100	4.00E-75	vacuolar adenosine triphosphatase subunit D (Mus musculus)
239	U:053488.46:2001MAY17	g3712671	1.00E-136	vascular endothelial growth factor (Homo sapiens)
240	U:058298.27:2001MAY17	g17045994	1.00E-100	unnamed protein product (Homo sapiens)
241	U:1110046.1:2001MAY17	g1854374	1.00E-172	aquaporin 3 (Homo sapiens)
242	U:1166752.11:2001MAY17	g15929737	1.00E-131	Similar to zinc finger protein 347 (Mus musculus)
243	U:1173766.1:2001MAY17	g7239109	0	HSPC059 (Homo sapiens)
244	U:1177952.4:2001MAY17	g14042590	1.00E-116	unnamed protein product (Homo sapiens)
245	U:1178064.3:2001MAY17	g5262591	0	hypothetical protein (Homo sapiens)
246	U:1183121.1:2001MAY17	g15489325	1.00E-163	Similar to hypothetical protein MGC10520 (Homo sapiens)
247	U:1190431.13:2001MAY17	g451303	0	complement receptor 1 (Homo sapiens)
248	U:199121.14:2001MAY17	g15593660	0	unnamed protein product (synthetic construct)
249	U:202630.5:2001MAY17	g14134965	0	unnamed protein product (Homo sapiens)
250	U:2034488.1:2001MAY17	g15277259	1.00E-156	zinc finger protein homologous to mouse Zfp91 (Homo sapiens)
251	U:2051434.8:2001MAY17	g13436164	1.00E-151	carbonic anhydrase III, muscle specific (Homo sapiens)
252	U:2118475.9:2001MAY17	g37605	0	urokinase plasminogen activator receptor (Homo sapiens)
253	U:218849.24:2001MAY17	g4240249	0	KIAA0880 protein (Homo sapiens)
254	U:2199824.5:2001MAY17	g15929959	1.00E-105	Similar to tropomyosin 4 (Homo sapiens)
255	U:233018.32:2001MAY17	g15928921	0	hypothetical protein FLJ14393 (Homo sapiens)
256	U:236295.8:2001MAY17	g33967	1.00E-124	interferon regulatory factor-2 (AA 1-349) (Homo sapiens)
257	U:286989.14:2001MAY17	g2967646	0	Smad2 (Homo sapiens)
258	U:345320.4:2001MAY17	g2330595	0	Ikars transcription factor (Gallus gallus)
259	U:355693.18:2001MAY17	g961515	0	plexin (Xenopus laevis)
260	U:359876.1:2001MAY17	g15293713	1.00E-123	olfactory receptor (Homo sapiens)
261	U:406664.32:2001MAY17	g432656	0	serum response factor-related protein (Homo sapiens)
262	U:410324.1:2001MAY17	g14009459	0	protocadherin-beta 11 (Homo sapiens)
263	U:414376.12:2001MAY17	g199893	0	murine potassium channel protein (Mus musculus)
264	U:452089.1:2001MAY17	g7340874	4.00E-96	ESTs D15590(C0900), D48950(S15542), D22684(C0900) correspond to a region of the predicted gene. ~Similar to Arabidopsis thaliana 60S ribosomal protein L11A (L16A). (P42795) (Oryza sativa)

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
265	LI:481614.43:2001MAY17	g14522878	0	calcium/calmodulin-dependent protein kinase kinase b2 (Homo sapiens)
266	LI:809605.2:2001MAY17	g4096339	0	zinc finger protein (Homo sapiens)
267	LI:816437.25:2001MAY17	g475560	0	N-methyl-D-aspartate receptor NMDAR1-2b subunit (Rattus norvegicus)
268	LI:817827.5:2001MAY17	g2668738	3.00E-89	translation initiation factor 5A (Zea mays)
269	LI:002345.15:2001MAY17	g12405805	0	unnamed protein product (Homo sapiens)
270	LI:022629.5:2001MAY17	g13879442	1.00E-119	Similar to RIKEN cDNA 2310035M22 gene (Mus musculus)
271	LI:061031.4:2001MAY17	g1763638	1.00E-110	alpha1A-voltage-dependent calcium channel (Homo sapiens)
272	LI:108232.2:2001MAY17	g12837586	4.00E-64	putative (Mus musculus)
273	LI:1085493.16:2001MAY17	g14042544	1.00E-158	unnamed protein product (Homo sapiens)
274	LI:1085513.2:2001MAY17	g16307285	0	Unknown (protein for IMAGE:3877337) (Homo sapiens)
275	LI:1086797.9:2001MAY17	g14133251	0	KIAA1479 protein (Homo sapiens)
276	LI:1088446.1:2001MAY17	g13676461	0	hypothetical protein (Macaca fascicularis)
277	LI:1133764.3:2001MAY17	g5262574	0	hypothetical protein (Homo sapiens)
278	LI:1147614.5:2001MAY17	g17049366	0	unnamed protein product (Homo sapiens)
279	LI:1181710.1:2001MAY17	g7959207	2.00E-60	KIAA1473 protein (Homo sapiens)
280	LI:1183192.1:2001MAY17	g13938261	7.00E-91	Unknown (protein for MGC:15514) (Homo sapiens)
281	LI:1188786.15:2001MAY17	g7020611	0	unnamed protein product (Homo sapiens)
282	LI:145626.1:2001MAY17	g14787176	0	CSMD1 (Mus musculus)
283	LI:147869.3:2001MAY17	g16549477	0	unnamed protein product (Homo sapiens)
284	LI:151747.4:2001MAY17	g3643115	0	protein inhibitor of activated STAT protein PIASx-beta (Homo sapiens)
285	LI:198296.1:2001MAY17	g12853497	0	putative (Mus musculus)
286	LI:200117.4:2001MAY17	g13358646	2.00E-96	hypothetical protein (Macaca fascicularis)
287	LI:200704.1:2001MAY17	g16551759	0	unnamed protein product (Homo sapiens)
288	LI:2049995.3:2001MAY17	g6063017	0	tousled-like kinase 1 (Homo sapiens)
289	LI:2052097.2:2001MAY17	g13195460	0	putative acetyltransferase (Homo sapiens)
290	LI:209351.22:2001MAY17	g12856025	0	putative (Mus musculus)
291	LI:2120481.1:2001MAY17	g10800564	0	bA338L1.1 (novel CUB domain protein similar to attractin) (Homo sapiens)
292	LI:2121610.13:2001MAY17	g8919698	1.00E-113	olfactory receptor (Mus musculus)
293	LI:2191585.1:2001MAY17	g12846015	1.00E-169	putative (Mus musculus)
294	LI:2198562.3:2001MAY17	g3513571	1.00E-164	C-terminal binding protein 2 CtBP2 (Mus musculus)
295	LI:2209684.5:2001MAY17	g15020827	0	dJ29K1.2 (KIAA0426 (C2H2 type zinc finger protein)) (Homo sapiens)

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
296	LI:222795.28:2001MAY17	g14602998	0	Unknown (protein for IMAGE:4121355) (Homo sapiens)
297	LI:228273.25:2001MAY17	g11323324	0	dJ13887.3.2 (lethal (3) malignant brain tumor ((3)mbf) protein (Drosophila) homolog (isoform 2) (KIAA0681)) (Homo sapiens)
298	LI:232386.31:2001MAY17	g3142288	0	protein kinase C-binding protein RACK7 (Homo sapiens)
299	LI:233089.2:2001MAY17	g7242977	0	KIAA1311 protein (Homo sapiens)
300	LI:240641.10:2001MAY17	g7019901	0	unnamed protein product (Homo sapiens)
301	LI:243871.4:2001MAY17	g6729590	1.00E-110	Fas-associated factor, FAF1 (Homo sapiens)
302	LI:245597.7:2001MAY17	g63180	7.00E-57	p54 (c-ets) protein (AA 1-441) (Gallus gallus)
303	LI:256009.31:2001MAY17	g10445221	1.00E-74	GTP-binding protein SAR1 (Homo sapiens)
304	LI:262221.1:2001MAY17	g7959343	1.00E-161	KIAA1538 protein (Homo sapiens)
305	LI:332957.8:2001MAY17	g10434090	1.00E-141	unnamed protein product (Homo sapiens)
306	LI:335352.13:2001MAY17	g306487	1.00E-129	cap-binding protein (Homo sapiens)
307	LI:343844.7:2001MAY17	g5102580	9.00E-98	hypothetical protein, similar to (AF134804) putative zinc finger transcription factor OVO1 (Mus musculus) (Homo sapiens)
308	LI:344528.1:2001MAY17	g3256266	0	MTG8-related protein MTG16b (Homo sapiens)
309	LI:374578.27:2001MAY17	g2664429	0	hypothetical protein (Homo sapiens)
310	LI:381993.13:2001MAY17	g17223624	0	ATP-binding cassette A9 (Homo sapiens)
311	LI:400373.2:2001MAY17	g17386053	0	Jedi protein (Mus musculus)
312	LI:400963.6:2001MAY17	g6634025	0	KIAA0379 protein (Homo sapiens)
313	LI:404874.8:2001MAY17	g3253159	0	translation initiation factor eIF2C (Oryctolagus cuniculus)
314	LI:405158.18:2001MAY17	g6807862	0	hypothetical protein (Homo sapiens)
315	LI:405889.22:2001MAY17	g8885518	0	hypothetical protein (Mus musculus)
316	LI:411151.31:2001MAY17	g6969631	0	oracle 2 protein (Mus musculus)
317	LI:411313.51:2001MAY17	g4239984	0	insulin receptor substrate protein of 53 kDa (a shorter form) (Homo sapiens)
318	LI:417127.1:2001MAY17	g12652727	3.00E-43	Unknown (protein for IMAGE:3352566) (Homo sapiens)
319	LI:429817.44:2001MAY17	g10443902	1.00E-116	TESTIN 2 (Homo sapiens)
320	LI:474134.23:2001MAY17	g13516831	0	MAIL (Homo sapiens)
321	LI:475378.3:2001MAY17	g7243105	1.00E-118	KIAA1362 protein (Homo sapiens)
322	LI:749588.15:2001MAY17	g4185940	0	env protein (Human endogenous retrovirus K)
323	LI:757736.17:2001MAY17	g16550160	0	unnamed protein product (Homo sapiens)
324	LI:817278.4:2001MAY17	g13477159	2.00E-63	TLS-associated serine-arginine protein 2 (Homo sapiens)

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
325	LI:027320.5:2001MAY17	g12839186	0	putative (Mus musculus)
326	LI:204635.5:2001MAY17	g13311008	2.00E-11	Homo sapiens NYD-SP16 mRNA, complete cds.
327	LI:215532.38:2001MAY17	g12803351	0	Unknown (protein for IMAGE:3050476) (Homo sapiens)
328	LI:228319.6:2001MAY17	g16041142	1.00E-133	hypothetical protein (Macaca fascicularis)
329	LI:236589.24:2001MAY17	g17064170	0	HSV-1 stimulating-related protein (Homo sapiens)
330	LI:247444.3:2001MAY17	g13435476	1.00E-133	Unknown (protein for MGC:6708) (Mus musculus)
331	LI:332404.20:2001MAY17	g14388334	0	hypothetical protein (Macaca fascicularis)
332	LG:1088459.4:2001JUN22	g2306773	2.00E-21	zinc finger protein (Homo sapiens)
333	LG:1501495.1:2001JUN22	g38032	0	ZNF43 (Homo sapiens)
334	LG:334284.10:2001JUN22	g12855389	2.00E-41	putative (Mus musculus)
335	LG:345279.19:2001JUN22	g1199602	1.00E-115	cyclophilin-like protein (Homo sapiens)
336	LG:7689681.1:2001JUN22	g17511871	9.00E-96	Unknown (protein for MGC:32104) (Homo sapiens)
337	LG:7690093.1:2001JUN22	g38032	0	ZNF43 (Homo sapiens)
338	LG:7690175.3:2001JUN22	g12052983	1.00E-115	hypothetical protein (Homo sapiens)
339	LG:7697128.1:2001JUN22	g17511825	1.00E-70	Similar to immunoglobulin kappa constant (Homo sapiens)
340	LG:006394.20:2001JUN22	g6808105	3.00E-79	hypothetical protein (Homo sapiens)
341	LG:1012069.1:2001JUN22	g15451412	1.00E-105	hypothetical protein (Macaca fascicularis)
342	LG:104533.11:2001JUN22	g5050962	2.00E-29	dJ34821.5 (PUTATIVE novel protein with ZU5 domain similar to part of Tight Junction Protein ZO1 (TJP1) and UNC5 Homologs) (Homo sapiens)
343	LG:1045853.23:2001JUN22	g7297900	1.00E-132	CG6734 gene product (Drosophila melanogaster)
344	LG:1081017.8:2001JUN22	g7768736	1.00E-13	putative gene, ankirin like, possible dual specificity Ser/Thr/Tyr kinase domain (Homo sapiens)
345	LG:1090358.6:2001JUN22	g5080758	3.00E-16	BC331191_1 (Homo sapiens)
346	LG:1135312.7:2001JUN22	g14279194	0	aldo-keto reductase loopADR (Homo sapiens)
347	LG:1328501.2:2001JUN22	g16551783	1.00E-115	unnamed protein product (Homo sapiens)
348	LG:133095.1:2001JUN22	g16877077	0	Unknown (protein for MGC:24494) (Homo sapiens)
349	LG:135379.5:2001JUN22	g16552010	0	unnamed protein product (Homo sapiens)
350	LG:1365581.3:2001JUN22	g347906	8.00E-17	zinc finger protein (Homo sapiens)
351	LG:1383156.20:2001JUN22	g387030	1.00E-104	pulmonary surfactant protein SP-C1 (Homo sapiens)
352	LG:1501767.18:2001JUN22	g11611571	1.00E-115	hypothetical protein (Macaca fascicularis)
353	LG:1501890.8:2001JUN22	g7021971	0	unnamed protein product (Homo sapiens)

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
354	LG:203434.23:2001JUN22	g4902831	1.00E-65	put. keratin K7 (Homo sapiens)
355	LG:204724.5:2001JUN22	g209820	0	transformation-associated protein (Human adenovirus type 2)
356	LG:257107.16:2001JUN22	g9992893	0	phosphoinositol 3-phosphate binding protein-1 (Homo sapiens)
357	LG:353530.4:2001JUN22	g6329945	0	KIAA1140 protein (Homo sapiens)
358	LG:7683573.3:2001JUN22	g16550444	1.00E-27	unnamed protein product (Homo sapiens)
359	LG:7684224.1:2001JUN22	g487284	1.00E-130	CRP2 (cysteine-rich protein 2) (Rattus norvegicus)
360	LG:7690365.2:2001JUN22	g12052983	1.00E-176	hypothetical protein (Homo sapiens)
361	LG:968691.1:2001JUN22	g17105197	1.00E-120	kelch-like protein KLHL6 (Homo sapiens)
362	LG:983076.7:2001JUN22	g15559519	0	Unknown (protein for IMAGE:4561365) (Homo sapiens)
363	LG:986291.1:2001JUN22	g206734	1.00E-173	ribosomal protein L5 (Rattus norvegicus)
364	LG:990347.41:2001JUN22	g3327090	1.00E-118	KIAA0638 protein (Homo sapiens)
365	LG:998305.4:2001JUN22	g12314195	1.00E-120	bA255A11.3 (novel protein similar to KIAA1074) (Homo sapiens)
366	LG:463420.16:2001JUN22	g7959265	0	KIAA1502 protein (Homo sapiens)
367	LG:979059.3:2001JUN22	g15862442	0	unnamed protein product (Homo sapiens)
368	LG:1045509.22:2001JUN22	g12653241	1.00E-41	transmembrane 4 superfamily member 7 (Homo sapiens)
369	LG:246935.4:2001JUN22	g12232324	1.00E-162	hUPF38 (Homo sapiens)
370	LG:321069.2:2001JUN22	g12856090	1.00E-60	putative (Mus musculus)
371	LG:346724.14:2001JUN22	g508729	0	thymopoietin gamma (Homo sapiens)
372	LG:411043.3:2001JUN22	g12861800	0	putative (Mus musculus)
373	LG:978620.7:2001JUN22	g438007	2.00E-22	alpha-2-macroglobulin receptor (Gallus gallus)
374	LG:982784.1:2001JUN22	g16553391	1.00E-136	unnamed protein product (Homo sapiens)
375	LG:007574.21:2001JUN22	g4589670	0	KIAA1010 protein (Homo sapiens)
376	LG:013856.18:2001JUN22	g7307264	0	formin binding protein 30 (Mus musculus)
377	LG:027320.7:2001JUN22	g16553765	0	unnamed protein product (Homo sapiens)
378	LG:077967.9:2001JUN22	g12804209	0	Similar to spleen tyrosine kinase (Homo sapiens)
379	LG:128475.9:2001JUN22	g13516831	3.00E-26	MAIL (Homo sapiens)
380	LG:1398104.15:2001JUN22	g15072406	1.00E-102	TNFAIP1-like protein (Homo sapiens)
381	LG:1454018.10:2001JUN22	g15042611	0	Ser/Thr protein kinase PAR-1beta (Homo sapiens)
382	LG:221548.14:2001JUN22	g10437204	0	unnamed protein product (Homo sapiens)
383	LG:227500.5:2001JUN22	g16551917	0	unnamed protein product (Homo sapiens)
384	LG:228273.22:2001JUN22	g3811111	0	l(3)mbt protein homolog (Homo sapiens)

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
385	LG:235432.1:2001JUN22	g12655229	0	glucocorticoid modulatory element binding protein 1 (Homo sapiens)
386	LG:236904.20:2001JUN22	g6691099	0	SWAP-70 (Homo sapiens)
387	LG:253193.21:2001JUN22	g7578783	4.00E-44	HT015 protein (Homo sapiens)
388	LG:332161.3:2001JUN22	g16555334	1.00E-109	Rlg protein (Homo sapiens)
389	LG:332923.5:2001JUN22	g14388339	0	hypothetical protein (Macaca fascicularis)
390	LG:343500.27:2001JUN22	g12854500	3.00E-88	putative (Mus musculus)
391	LG:369703.9:2001JUN22	g16741627	0	Similar to RIKEN cDNA 3830421M04 gene (Homo sapiens)
392	LG:415378.3:2001JUN22	g11320820	0	VSGP/F-spondin (Homo sapiens)
393	LG:458583.1:2001JUN22	g7020724	9.00E-76	unnamed protein product (Homo sapiens)
394	LG:7690373.1:2001JUN22	g7959207	2.00E-60	KIAA1473 protein (Homo sapiens)
395	LG:898324.13:2001JUN22	g16551459	1.00E-100	unnamed protein product (Homo sapiens)
396	LG:979167.5:2001JUN22	g15788437	1.00E-131	cyclin-box carrying protein (Homo sapiens)



TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
1	LG:036272.1:2001MAR30	1664	2119	forward 2	Acyl-CoA_dh	Acyl-CoA dehydrogenase, C-terminal domain	4.90E-51
2	LG:093337.3:2001MAR30	245	367	forward 2	KRAB	KRAB box	2.10E-25
3	LG:1049927.6:2001MAR30	297	584	forward 3	SCAN	SCAN domain	7.50E-61
4	LG:1051891.34:2001MAR30	916	984	forward 1	zf-C2H2	Zinc finger, C2H2 type	4.10E-07
5	LG:1089626.1:2001MAR30	861	929	forward 3	zf-C2H2	Zinc finger, C2H2 type	3.80E-08
6	LG:1101416.6:2001MAR30	283	531	forward 1	Ribosomal_L7Ae	Ribosomal protein L7Ae/L30e/S12e/Gadd45 family	1.20E-21
7	LG:1295974.1:2001MAR30	185	655	forward 2	ferritin	Ferritin	9.00E-113
8	LG:1400572.2:2001MAR30	147	215	forward 3	zf-C2H2	Zinc finger, C2H2 type	2.30E-05
9	LG:1446621.1:2001MAR30	405	527	forward 3	KRAB	KRAB box	4.00E-23
10	LG:1499752.1:2001MAR30	67	189	forward 1	Thymosin	Thymosin beta-4 family	1.80E-24
11	LG:1503044.7:2001MAR30	367	441	forward 1	zf-A20	A20-like zinc finger	7.20E-11
12	LG:1503588.1:2001MAR30	130	252	forward 1	KRAB	KRAB box	4.00E-23
13	LG:1503589.2:2001MAR30	861	929	forward 3	zf-C2H2	Zinc finger, C2H2 type	2.00E-07
13	LG:1503589.2:2001MAR30	64	132	forward 1	zf-C2H2	Zinc finger, C2H2 type	4.90E-07
14	LG:1506339.4:2001MAR30	101	514	forward 2	Ribosomal_S5	Ribosomal protein S5	2.10E-87
15	LG:220648.6:2001MAR30	285	503	forward 3	UPAR_LY6	u-PAR/Ly-6 domain	3.20E-19
16	LG:236654.1:2001MAR30	820	888	forward 1	zf-C2H2	Zinc finger, C2H2 type	1.20E-04
17	LG:237699.26:2001MAR30	228	515	forward 3	Bcl-2	Apoptosis regulator proteins, Bcl-2 family	1.90E-42
18	LG:311541.16:2001MAR30	866	1222	forward 2	lectin_c	Lectin C-type domain	9.40E-19
18	LG:311541.16:2001MAR30	8	493	forward 2	SCP	SCP-like extracellular protein	7.20E-06
19	LG:335923.7:2001MAR30	53	400	forward 2	lys	C-type lysozyme/alpha-lactalbumin family	2.30E-40
20	LG:350342.14:2001MAR30	150	860	forward 3	pkinase	Protein kinase domain	1.30E-12
21	LG:369301.32:2001MAR30	454	789	forward 1	PX	PX domain	3.50E-10
22	LG:452089.1:2001MAR30	107	268	forward 2	Ribosomal_L5	Ribosomal protein L5	6.10E-26
22	LG:452089.1:2001MAR30	278	577	forward 2	Ribosomal_L5_C	ribosomal L5P family C-terminus	2.60E-59
23	LG:454087.3:2001MAR30	181	303	forward 1	KRAB	KRAB box	3.30E-25
23	LG:454087.3:2001MAR30	754	822	forward 1	zf-C2H2	Zinc finger, C2H2 type	1.80E-06
24	LG:466302.1:2001MAR30	79	486	forward 1	Ribosomal_L22	Ribosomal protein L22p/L17e	4.10E-68
25	LG:474267.1:2001MAR30	513	581	forward 3	MORN	MORN repeat	2.10E-08
26	LG:995613.10:2001MAR30	1342	1470	forward 1	ldl_recept_b	Low-density lipoprotein receptor repeat class B	1.10E-07
27	LG:011843.5:2001MAR30	1599	1928	forward 3	CUB	CUB domain	3.90E-17

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hlf	Pfam Description	E-value
27	LG:011843.5:2001MAR30	303	410	forward 3	EGF	EGF-like domain	2.30E-05
28	LG:075904.32:2001MAR30	1263	1601	forward 3	RA	Ras association (RalGDS/AF-6) domain	4.60E-09
29	LG:1004781.3:2001MAR30	637	804	forward 1	sushi	Sushi domain (SCR repeat)	5.20E-14
30	LG:1041807.8:2001MAR30	3	335	forward 3	RhoGAP	RhoGAP domain	2.60E-06
31	LG:1044448.2:2001MAR30	1821	1919	forward 3	ank	Ankyrin repeat	3.50E-08
32	LG:1080598.9:2001MAR30	315	437	forward 3	KRAB	KRAB box	1.80E-22
32	LG:1080598.9:2001MAR30	1119	1187	forward 3	zf-C2H2	Zinc finger, C2H2 type	2.30E-06
33	LG:1081017.1:2001MAR30	386	484	forward 2	ank	Ankyrin repeat	6.20E-08
34	LG:1083120.2:2001MAR30	77	199	forward 2	KRAB	KRAB box	1.20E-24
34	LG:1083120.2:2001MAR30	707	775	forward 2	zf-C2H2	Zinc finger, C2H2 type	2.50E-06
35	LG:1097492.12:2001MAR30	707	1255	forward 2	RhoGEF	RhoGEF domain	2.70E-33
36	LG:118834.9:2001MAR30	139	957	forward 1	Glyco_transf_8	Glycosyl transferase family 8	2.30E-04
37	LG:1227408.25:2001MAR30	986	1096	forward 2	WD40	WD domain, G-beta repeat	2.90E-07
38	LG:1326953.1:2001MAR30	1	360	forward 1	Ribosomal_L10e	Ribosomal L10	1.10E-07
39	LG:1397821.17:2001MAR30	210	989	forward 3	pkinase	Protein kinase domain	5.00E-14
40	LG:1512507.1:2001MAR30	305	469	forward 2	HTH_3	Helix-turn-helix	1.20E-10
41	LG:196583.5:2001MAR30	602	757	forward 2	tsp_1	Thrombospondin type 1 domain	3.80E-08
42	LG:198669.1:2001MAR30	65	187	forward 2	chromo	'chromo' (Chromatin Organization Modifier) domain	1.40E-16
43	LG:202943.1:2001MAR30	235	339	forward 1	EGF	EGF-like domain	1.60E-05
43	LG:202943.1:2001MAR30	1426	1587	forward 1	sushi	Sushi domain (SCR repeat)	3.80E-18
44	LG:204724.3:2001MAR30	3	482	forward 3	Adeno_E1B_19K	Adenovirus E1B 19K protein / small t-antigen	2.80E-95
44	LG:204724.3:2001MAR30	611	1762	forward 2	Adeno_E1B_55K	Adenovirus E1B 55K protein / large t-antigen	4.80E-260
45	LG:206425.10:2001MAR30	472	1299	forward 1	GBP	Guanylate-binding protein, N-terminal domain	5.40E-189
45	LG:206425.10:2001MAR30	1303	2178	forward 1	GBP_C	Guanylate-binding protein, C-terminal domain	2.30E-115
46	LG:208190.2:2001MAR30	181	303	forward 1	KRAB	KRAB box	4.50E-24
46	LG:208190.2:2001MAR30	1042	1110	forward 1	zf-C2H2	Zinc finger, C2H2 type	4.80E-07
47	LG:222927.2:2001MAR30	418	702	forward 1	Fork_head	Fork head domain	9.70E-27
48	LG:228046.5:2001MAR30	846	914	forward 3	zf-C2H2	Zinc finger, C2H2 type	9.10E-05
49	LG:230980.1:2001MAR30	211	309	forward 1	ank	Ankyrin repeat	4.50E-10
50	LG:236976.2:2001MAR30	336	506	forward 3	homeobox	Homeobox domain	5.50E-23
51	LG:238322.6:2001MAR30	536	1519	forward 2	Sema	Sema domain	1.20E-21

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hlft	Pfam Description	E-value
51	LG:238322.6:2001MAR30	706	1668	forward 1	Sema	Sema domain	1.20E-05
52	LG:341461.1:2001MAR30	288	485	forward 3	DnaJ	DnaJ domain	3.90E-35
53	LG:354088.1:2001MAR30	135	587	forward 3	ve	Integrase core domain	2.80E-21
54	LG:376275.1:2001MAR30	709	831	forward 1	KRAB	KRAB box	1.80E-24
55	LG:399281.3:2001MAR30	654	752	forward 3	ank	Ankyrin repeat	3.20E-09
55	LG:399281.3:2001MAR30	1618	1716	forward 1	ank	Ankyrin repeat	6.80E-06
56	LG:404921.10:2001MAR30	2555	2653	forward 2	ank	Ankyrin repeat	1.20E-10
56	LG:404921.10:2001MAR30	917	1231	forward 2	VPS9	Vacuolar sorting protein 9 (VPS9) domain	2.50E-12
57	LG:444677.34:2001MAR30	395	817	forward 2	FAA_hydrolase	Fumarylacetoacetate (FAA) hydrolase family	2.00E-26
58	LG:968691.1:2001MAR30	208	531	forward 1	BTB	BTB/POZ domain	2.40E-30
59	LG:983862.1:2001MAR30	226	399	forward 1	PBD	P21-Rho-binding domain	1.00E-08
59	LG:983862.1:2001MAR30	1411	2166	forward 1	pkinese	Protein kinase domain	1.40E-80
60	LG:984130.1:2001MAR30	302	625	forward 2	BTB	BTB/POZ domain	6.90E-33
60	LG:984130.1:2001MAR30	1196	1348	forward 2	Keich	Keich motif	3.10E-08
61	LG:986291.1:2001MAR30	127	570	forward 1	Ribosomal_L18p	Ribosomal L18p/L5e family	4.10E-74
62	LG:045210.8:2001MAR30	115	192	forward 1	RPEL	RPEL repeat	1.10E-06
63	LG:229284.39:2001MAR30	1914	2792	forward 3	TTL	Tubulin-tyrosine ligase family	1.90E-124
64	LG:337810.20:2001MAR30	227	355	forward 2	Armadillo_seg	Armadillo/beta-catenin-like repeat	1.50E-04
65	LG:463420.1:2001MAR30	2441	2995	forward 2	Glyco_transf_25	Glycosyltransferase family 25 (LPS biosynthesis protein)	2.00E-72
66	LG:1080918.1:2001MAR30	1003	1071	forward 1	zf-C2H2	Zinc finger, C2H2 type	2.90E-07
67	LG:1093747.15:2001MAR30	540	662	forward 3	KRAB	KRAB box	4.00E-22
67	LG:1093747.15:2001MAR30	1113	1181	forward 3	zf-C2H2	Zinc finger, C2H2 type	2.30E-07
68	LG:1096896.47:2001MAR30	185	601	forward 2	succ_DH_flav_C	Fumarate reductase/succinate dehydrogenase flavoprotein C-terminal	8.30E-60
69	LG:1098931.39:2001MAR30	1615	1902	forward 1	Biotin_carb_C	Biotin carboxylase C-terminal domain	1.00E-10
69	LG:1098931.39:2001MAR30	1694	1864	forward 2	Biotin_carb_C	Biotin carboxylase C-terminal domain	7.70E-04
69	LG:1098931.39:2001MAR30	2314	2514	forward 1	biotin_lipoyl	Biotin-requiring enzyme	2.30E-22
69	LG:1098931.39:2001MAR30	5012	6721	forward 2	Carboxyl_trans	Carboxyl transferase domain	9.30E-301
69	LG:1098931.39:2001MAR30	524	895	forward 2	CPSase_L_chain	Carbamoyl-phosphate synthase L chain, N-terminal domain	1.00E-57

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
69	LG:1098931.39:2001MAR30	899	1675	forward 2	CPSase_L_D2	Carbamoyl-phosphate synthase L chain, ATP binding domain	5.00E-142
70	LG:1100823.1:2001MAR30	88	792	forward 1	transmembrane4	Tetraspanin family	7.00E-07
70	LG:1100823.1:2001MAR30	197	733	forward 2	transmembrane4	Tetraspanin family	1.80E-06
71	LG:1166387.1:2001MAR30	731	958	forward 2	WWE	WWE domain	6.40E-20
71	LG:1166387.1:2001MAR30	563	676	forward 2	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	4.70E-04
72	LG:1383036.49:2001MAR30	333	545	forward 3	rrm	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	1.30E-23
73	LG:1452353.14:2001MAR30	3974	4501	forward 2	RasGAP	GTPase-activator protein for Ras-like GTPase	2.90E-102
74	LG:1452435.15:2001MAR30	2148	2246	forward 3	ank	Ankyrin repeat	2.90E-11
74	LG:1452435.15:2001MAR30	310	408	forward 1	ank	Ankyrin repeat	3.80E-10
74	LG:1452435.15:2001MAR30	869	967	forward 2	ank	Ankyrin repeat	9.10E-07
74	LG:1452435.15:2001MAR30	4260	4511	forward 3	death	Death domain	4.80E-25
74	LG:1452435.15:2001MAR30	2781	3095	forward 3	ZU5	ZU5 domain	5.70E-62
75	LG:1498774.1:2001MAR30	329	538	forward 2	elf-5a	Eukaryotic Initiation factor 5A hypusine, DNA-binding OB fold	3.40E-36
75	LG:1498774.1:2001MAR30	101	325	forward 2	elf-5a_N	Eukaryotic Initiation factor 5A hypusine, SH3-like barrel domain	2.30E-50
76	LG:197180.1:2001MAR30	66	554	forward 3	GTP_EFTU	Elongation factor Tu GTP binding domain	5.40E-08
76	LG:197180.1:2001MAR30	40	504	forward 1	GTP_EFTU	Elongation factor Tu GTP binding domain	7.60E-06
76	LG:197180.1:2001MAR30	864	1154	forward 3	GTP_EFTU_D3	Elongation factor Tu C-terminal domain	1.30E-40
77	LG:199489.1:2001MAR30	257	1810	forward 2	aa_permeases	Amino acid permease	1.20E-07
78	LG:201908.3:2001MAR30	274	396	forward 1	KRAB	KRAB box	3.80E-10
78	LG:201908.3:2001MAR30	2194	2262	forward 1	zf-C2H2	Zinc finger, C2H2 type	2.20E-06
79	LG:247245.26:2001MAR30	434	556	forward 2	KRAB	KRAB box	8.00E-21
79	LG:247245.26:2001MAR30	1364	1432	forward 2	zf-C2H2	Zinc finger, C2H2 type	1.60E-06
80	LG:256365.2:2001MAR30	480	1151	forward 3	Tropomyosin	Tropomyosin	1.50E-58
80	LG:256365.2:2001MAR30	458	1189	forward 2	Tropomyosin	Tropomyosin	6.20E-08
81	LG:332923.4:2001MAR30	1845	2114	forward 3	cadherin	Cadherin domain	1.00E-23
82	LG:335276.1:2001MAR30	726	896	forward 3	homeobox	Homeobox domain	1.30E-27
83	LG:350272.2:2001MAR30	562	930	forward 1	SPRY	SPRY domain	1.10E-10
84	LG:350921.2:2001MAR30	1388	1648	forward 2	UCH-2	Ubiquitin carboxyl-terminal hydrolase family 2	7.50E-16

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
85	LG:406568.1:2001MAR30	211	1197	forward 1	Tropomodulin	Tropomodulin	9.30E-91
86	LG:411043.3:2001MAR30	213	1199	forward 3	adh_zinc	Zinc-binding dehydrogenase	1.00E-19
87	LG:414376.20:2001MAR30	1637	2224	forward 2	lon_trans	Ion transport protein	6.60E-44
87	LG:414376.20:2001MAR30	976	1272	forward 1	K_tetra	K+ channel tetramerisation domain	2.40E-46
88	LG:457695.1:2001MAR30	278	436	forward 2	Ribosomal_L30	Ribosomal protein L30p/L7e	3.80E-23
89	LG:902390.2:2001MAR30	44	298	forward 2	ACBP	Acyl CoA binding protein	1.70E-46
90	LG:903565.20:2001MAR30	1288	1704	forward 1	P	Protein kinase P-domain	2.60E-77
90	LG:903565.20:2001MAR30	306	1529	forward 3	Peptidase_S8	Subtilase family	3.70E-63
90	LG:903565.20:2001MAR30	538	1254	forward 1	Peptidase_S8	Subtilase family	1.40E-05
91	LG:978182.4:2001MAR30	215	925	forward 2	Metallophos	Calcineurin-like phosphoesterase	4.30E-22
92	LG:986827.1:2001MAR30	104	673	forward 2	arf	ADP-ribosylation factor family	2.60E-11
93	LG:013792.1:2001MAR30	620	742	forward 2	KRAB	KRAB box	3.00E-21
94	LG:018258.1:2001MAR30	299	730	forward 2	Nitroreductase	Nitroreductase family	9.00E-05
95	LG:023126.3:2001MAR30	469	852	forward 1	ras	Ras family	1.50E-07
96	LG:023618.1:2001MAR30	237	479	forward 3	Acetyltransf	Acetyltransferase (GNAT) family	1.90E-17
97	LG:030999.1:2001MAR30	16	576	forward 1	arf	ADP-ribosylation factor family	5.60E-04
97	LG:030999.1:2001MAR30	670	867	forward 1	DnaJ	DnaJ domain	2.90E-09
97	LG:030999.1:2001MAR30	73	627	forward 1	ras	Ras family	6.70E-29
98	LG:103508.1:2001MAR30	771	1346	forward 3	Galactosyl_T	Galactosyltransferase	1.30E-40
99	LG:107976.15:2001MAR30	3214	3438	forward 1	PDZ	PDZ domain (Also known as DHR or GLGF).	5.90E-05
99	LG:107976.15:2001MAR30	2441	3007	forward 2	Rap_GAP	Rap/ran-GAP	2.30E-133
100	LG:1080096.1:2001MAR30	1708	1776	forward 1	zf-C2H2	Zinc finger, C2H2 type	1.70E-07
101	LG:1080275.1:2001MAR30	550	618	forward 1	zf-C2H2	Zinc finger, C2H2 type	2.20E-06
102	LG:1090358.10:2001MAR30	781	903	forward 1	KRAB	KRAB box	3.90E-27
102	LG:1090358.10:2001MAR30	1425	1493	forward 3	zf-C2H2	Zinc finger, C2H2 type	2.70E-07
102	LG:1090358.10:2001MAR30	1258	1326	forward 1	zf-C2H2	Zinc finger, C2H2 type	7.70E-07
103	LG:1095833.9:2001MAR30	1655	1948	forward 2	TIG	IPT/TIG domain	1.30E-16
104	LG:1383121.25:2001MAR30	106	807	forward 1	DEAD	DEAD/DEAH box helicase	2.60E-09
104	LG:1383121.25:2001MAR30	1587	1805	forward 3	helicase_C	Helicase conserved C-terminal domain	2.80E-28
105	LG:1386609.2:2001MAR30	638	823	forward 2	UCH-2	Ubiquitin carboxyl-terminal hydrolase family 2	9.50E-27
106	LG:1398465.1:2001MAR30	2392	2502	forward 1	WD40	WD domain, G-beta repeat	6.80E-10
106	LG:1398465.1:2001MAR30	83	196	forward 2	WD40	WD domain, G-beta repeat	5.10E-08

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
107	LG:1453417.10:2001MAR30	7031	7762	forward 2	7tm_2	7 transmembrane receptor (Secretin family)	4.10E-57
107	LG:1453417.10:2001MAR30	1124	1402	forward 2	cadherin	Cadherin domain	3.30E-28
107	LG:1453417.10:2001MAR30	4646	4741	forward 2	EGF	EGF-like domain	7.40E-08
107	LG:1453417.10:2001MAR30	6857	7018	forward 2	GPS	Latrophillin/CL-1-like GPS domain	1.50E-27
107	LG:1453417.10:2001MAR30	5831	6004	forward 2	HRM	Hormone receptor domain	1.60E-17
107	LG:1453417.10:2001MAR30	5684	5821	forward 2	laminin_EGF	Laminin EGF-like (Domains III and V)	5.20E-11
107	LG:1453417.10:2001MAR30	4097	4585	forward 2	laminin_G	Laminin G domain	1.00E-14
108	LG:147869.3:2001MAR30	1	2034	forward 1	Patched	Patched family	3.60E-13
109	LG:148485.5:2001MAR30	54	857	forward 3	FGGY	FGGY family of carbohydrate kinases, N-terminal domain	4.10E-36
110	LG:1501818.12:2001MAR30	306	1172	forward 3	cobw	Cobalamin synthesis protein/P47K	3.70E-53
111	LG:1508275.1:2001MAR30	194	280	forward 2	efhand	EF hand	5.40E-04
111	LG:1508275.1:2001MAR30	47	178	forward 2	S_100	S-100/CaBP type calcium binding domain	3.60E-23
112	LG:1509771.1:2001MAR30	67	384	forward 1	Rhodanese	Rhodanese-like domain	1.10E-13
113	LG:1512998.13:2001MAR30	859	1053	forward 1	FYVE	FYVE zinc finger	2.50E-27
114	LG:198251.7:2001MAR30	293	397	forward 2	G-gamma	GGL domain	2.80E-09
115	LG:198296.1:2001MAR30	646	783	forward 1	Kelch	Kelch motif	5.50E-14
116	LG:198876.13:2001MAR30	343	813	forward 1	Anti_proliferat	BTG1 family	2.20E-101
117	LG:200704.1:2001MAR30	862	1044	forward 1	ig	Immunoglobulin domain	3.00E-06
118	LG:206593.3:2001MAR30	704	772	forward 2	zf-C2H2	Zinc finger, C2H2 type	1.30E-07
118	LG:206593.3:2001MAR30	295	363	forward 1	zf-C2H2	Zinc finger, C2H2 type	7.00E-07
118	LG:206593.3:2001MAR30	222	290	forward 3	zf-C2H2	Zinc finger, C2H2 type	1.10E-06
119	LG:223970.11:2001MAR30	492	695	forward 3	rrm	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	3.70E-09
120	LG:227500.5:2001MAR30	869	1042	forward 2	LIM	LIM domain	5.80E-11
121	LG:227722.7:2001MAR30	2	472	forward 2	AAA	ATPase family associated with various cellular activities (AAA)	3.10E-21
122	LG:229105.1:2001MAR30	84	323	forward 3	heme_1	Heme/Steroid binding domain	4.60E-16
123	LG:233761.4:2001MAR30	1200	1562	forward 3	SPRY	SPRY domain	2.90E-12
123	LG:233761.4:2001MAR30	315	440	forward 3	zf-B_box	B-box zinc finger.	4.70E-12
123	LG:233761.4:2001MAR30	107	229	forward 2	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	8.20E-13
124	LG:234326.67:2001MAR30	3134	3709	forward 2	Reticulon	Reticulon	4.00E-107

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
125	LG:236056.27:2001MAR30	1003	1242	forward 1	SWIB	BAF60b domain of the SWIB complex	1.20E-23
126	LG:253889.31:2001MAR30	404	619	forward 2	rrm	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	6.40E-26
127	LG:270833.135:2001MAR30	78	290	forward 3	RNA_pol_L	RNA polymerases L / 13 to 16 kDa subunit	2.90E-21
128	LG:292613.7:2001MAR30	1206	1346	forward 3	PHD	PHD-finger	3.60E-06
129	LG:331546.2:2001MAR30	241	1038	forward 1	PP2C	Protein phosphatase 2C	4.40E-57
130	LG:332027.6:2001MAR30	660	1643	forward 3	Methyltransf_5	MraW methylase family	1.00E-90
131	LG:336998.1:2001MAR30	4500	4679	forward 3	PHD	PHD-finger	5.20E-11
131	LG:336998.1:2001MAR30	11241	11627	forward 3	SET	SET domain	1.30E-61
131	LG:336998.1:2001MAR30	3237	3380	forward 3	zf-CXXC	CXXC zinc finger	9.70E-24
132	LG:338010.8:2001MAR30	524	718	forward 2	zf-DHHC	DHHC zinc finger domain	6.70E-27
133	LG:344597.1:2001MAR30	1174	1500	forward 1	CUB	CUB domain	3.00E-15
133	LG:344597.1:2001MAR30	1525	1692	forward 1	sushi	Sushi domain (SCR repeat)	1.30E-14
134	LG:347361.2:2001MAR30	2254	2352	forward 1	ank	Ankyrin repeat	1.20E-11
134	LG:347361.2:2001MAR30	1497	1595	forward 3	ank	Ankyrin repeat	1.50E-07
134	LG:347361.2:2001MAR30	201	515	forward 3	BTB	BTB/POZ domain	9.00E-13
134	LG:347361.2:2001MAR30	3253	3444	forward 1	FYVE	FYVE zinc finger	7.00E-21
135	LG:349293.17:2001MAR30	1908	2018	forward 3	WD40	WD domain, G-beta repeat	2.90E-08
136	LG:410595.19:2001MAR30	727	1029	forward 1	CH	Calponin homology (CH) domain	8.70E-06
137	LG:411151.35:2001MAR30	1548	1718	forward 3	LIM	LIM domain	3.90E-14
137	LG:411151.35:2001MAR30	60	299	forward 3	PDZ	PDZ domain (Also known as DHR or GLGF).	1.50E-17
138	LG:411334.8:2001MAR30	1680	1856	forward 3	LIM	LIM domain	2.70E-11
139	LG:458583.1:2001MAR30	31	141	forward 1	WD40	WD domain, G-beta repeat	4.60E-08
140	LG:475378.1:2001MAR30	1936	2133	forward 1	FYVE	FYVE zinc finger	1.50E-15
140	LG:475378.1:2001MAR30	1567	1848	forward 1	PH	PH domain	4.40E-13
140	LG:475378.1:2001MAR30	913	1476	forward 1	RhoGEF	RhoGEF domain	2.40E-07
141	LG:481572.1:2001MAR30	502	858	forward 1	Alpp	Appr-1"-p processing enzyme family	1.10E-31
141	LG:481572.1:2001MAR30	2492	2728	forward 2	WWE	WWE domain	3.20E-23
142	LG:481704.1:2001MAR30	114	575	forward 3	rve	Integrase core domain	3.40E-34
143	LG:898195.4:2001MAR30	365	688	forward 2	BTB	BTB/POZ domain	4.00E-42
143	LG:898195.4:2001MAR30	1397	1534	forward 2	Kelch	Kelch motif	7.50E-17
144	LG:903785.1:2001MAR30	210	629	forward 3	DSPc	Dual specificity phosphatase, catalytic	6.60E-37

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hlt	Pfam Description	E-value
145	LG:977454.3:2001MAR30	10	327	forward 1	GSHPx	Glutathione peroxidase	1.70E-19
146	LG:977724.12:2001MAR30	1606	1776	forward 1	SH3	SH3 domain	1.70E-16
146	LG:977724.12:2001MAR30	298	420	forward 1	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	5.20E-07
147	LG:978215.19:2001MAR30	1050	1199	forward 3	LRRCT	Leucine rich repeat C-terminal domain	4.80E-10
148	LG:981795.1:2001MAR30	265	807	forward 1	PMP22_Claudin	PMP-22/EMP/MP20/Claudin family	3.10E-05
149	LG:982784.1:2001MAR30	582	650	forward 3	zf-C2H2	Zinc finger, C2H2 type	2.90E-05
150	LG:987322.4:2001MAR30	863	1423	forward 2	SIR2	Sir2 family	4.10E-100
151	LG:006242.7:2001MAR30	87	443	forward 3	DUF232	Putative transcriptional regulator	2.00E-27
152	LG:027320.7:2001MAR30	158	358	forward 2	SAM	SAM domain (Sterile alpha motif)	6.30E-06
153	LG:147541.44:2001MAR30	106	849	forward 1	DUF259	Protein of unknown function, DUF259	2.90E-04
154	LG:228319.2:2001MAR30	811	1032	forward 1	mbf	mbf repeat	6.30E-39
155	LG:238754.19:2001MAR30	205	534	forward 1	Ylppee	Ylppee putative zinc-binding protein	8.70E-69
156	LG:405751.12:2001MAR30	1241	1582	forward 2	MA3	MA3 domain	4.30E-46
157	LI:011822.6:2001MAY17	306	1199	forward 3	kinesin	Kinesin motor domain	5.90E-142
158	LI:1012467.2:2001MAY17	27	827	forward 3	pkinase	Protein kinase domain	7.30E-76
159	LI:1169981.13:2001MAY17	104	226	forward 2	KRAB	KRAB box	1.30E-24
159	LI:1169981.13:2001MAY17	1031	1099	forward 2	zf-C2H2	Zinc finger, C2H2 type	8.60E-07
160	LI:1171553.1:2001MAY17	1389	1457	forward 3	zf-C2H2	Zinc finger, C2H2 type	3.80E-08
161	LI:1183156.3:2001MAY17	395	517	forward 2	KRAB	KRAB box	1.50E-26
161	LI:1183156.3:2001MAY17	1247	1315	forward 2	zf-C2H2	Zinc finger, C2H2 type	2.40E-07
161	LI:1183156.3:2001MAY17	2034	2102	forward 3	zf-C2H2	Zinc finger, C2H2 type	1.70E-05
162	LI:1188500.6:2001MAY17	195	782	forward 3	AAA	ATPase family associated with various cellular activities (AAA)	1.60E-44
163	LI:147333.12:2001MAY17	1259	1675	forward 2	Dak1	Dak1 domain	8.60E-07
164	LI:147523.7:2001MAY17	99	554	forward 3	sodcu	Copper/zinc superoxide dismutase (SODC)	8.10E-104
165	LI:197388.10:2001MAY17	323	820	forward 2	lactamase_B	Metallo-beta-lactamase superfamily	2.90E-35
166	LI:2049216.1:2001MAY17	614	712	forward 2	ank	Ankyrin repeat	5.60E-09
166	LI:2049216.1:2001MAY17	137	499	forward 2	ArfGap	Putative GTP-ase activating protein for Arf	1.60E-48
167	LI:2051624.2:2001MAY17	105	1007	forward 3	PALP	Pyridoxal-phosphate dependent enzyme	5.00E-65
168	LI:2121838.1:2001MAY17	426	494	forward 3	zf-C2H2	Zinc finger, C2H2 type	2.40E-07
169	LI:2122954.8:2001MAY17	309	431	forward 3	KRAB	KRAB box	1.70E-18
169	LI:2122954.8:2001MAY17	967	1035	forward 1	zf-C2H2	Zinc finger, C2H2 type	1.30E-06



TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
170	U:2198064.2:2001MAY17	96	164	forward 3	zf-C2H2	Zinc finger, C2H2 type	1.50E-06
171	U:2206583.1:2001MAY17	368	436	forward 2	zf-C2H2	Zinc finger, C2H2 type	1.90E-06
171	U:2206583.1:2001MAY17	237	305	forward 3	zf-C2H2	Zinc finger, C2H2 type	9.90E-06
172	U:235663.6:2001MAY17	195	767	forward 3	Galactosyl_T	Galactosyltransferase	7.60E-20
173	U:236386.7:2001MAY17	1430	1759	forward 2	PX	PX domain	3.10E-22
173	U:236386.7:2001MAY17	766	936	forward 1	SH3	SH3 domain	1.20E-11
174	U:236654.3:2001MAY17	816	884	forward 3	zf-C2H2	Zinc finger, C2H2 type	1.20E-04
175	U:256059.46:2001MAY17	205	741	forward 1	MHC_J	Class I Histocompatibility antigen, domains alpha 1 and 2	4.20E-139
176	U:279978.22:2001MAY17	137	1372	forward 2	AMP-binding	AMP-binding enzyme	4.80E-94
177	U:311541.6:2001MAY17	2166	2417	forward 3	lectin_c	Lectin C-type domain	2.90E-04
177	U:311541.6:2001MAY17	273	806	forward 3	SCP	SCP-like extracellular protein	2.00E-12
178	U:346123.1:2001MAY17	95	841	forward 2	TIM	Triosephosphate isomerase	6.80E-176
179	U:381211.5:2001MAY17	626	748	forward 2	KRAB	KRAB box	1.60E-22
179	U:381211.5:2001MAY17	1281	1349	forward 3	zf-C2H2	Zinc finger, C2H2 type	1.10E-07
179	U:381211.5:2001MAY17	2165	2233	forward 2	zf-C2H2	Zinc finger, C2H2 type	1.60E-07
180	U:412197.82:2001MAY17	1331	1819	forward 2	Ribosomal_S5	Ribosomal protein S5	1.90E-63
181	U:412936.49:2001MAY17	343	435	forward 1	WW	WW domain	2.40E-06
182	U:427792.139:2001MAY17	3	338	forward 3	Peptidase_C1	Papain family cysteine protease	2.20E-05
183	U:450229.1:2001MAY17	85	648	forward 1	Ribosomal_S7e	Ribosomal protein S7e	4.60E-83
184	U:475565.243:2001MAY17	75	197	forward 3	KRAB	KRAB box	2.20E-22
185	U:764701.8:2001MAY17	866	1345	forward 2	Peptidase_S26	Signal peptidase I	4.60E-58
186	U:024124.2:2001MAY17	531	773	forward 3	Ig	Immunoglobulin domain	5.40E-06
186	U:024124.2:2001MAY17	822	1106	forward 3	Xlink	Extracellular link domain	3.30E-43
187	U:038252.3:2001MAY17	2887	3480	forward 1	STAT_bind	STAT protein, DNA binding domain	3.60E-76
188	U:056882.1:2001MAY17	313	435	forward 1	KRAB	KRAB box	1.80E-24
189	U:059530.1:2001MAY17	2039	2107	forward 2	GoLoco	LGN motif, putative GEF specific for G-alpha GTPase	5.20E-08
190	U:089950.30:2001MAY17	1008	1265	forward 3	C2	C2 domain	1.60E-26
191	U:1072906.38:2001MAY17	890	979	forward 2	WW	WW domain	7.30E-08
192	U:1158936.4:2001MAY17	280	393	forward 1	WD40	WD domain, G-beta repeat	5.80E-09
193	U:1173412.15:2001MAY17	1160	1918	forward 2	UPF0034	Uncharacterized protein family UPF0034	2.50E-09

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
194	LI:1174279.14:2001MAY17	276	398	forward 3	KRAB	KRAB box	3.50E-26
194	LI:1174279.14:2001MAY17	1008	1076	forward 3	zf-C2H2	Zinc finger, C2H2 type	2.70E-07
195	LI:1174809.1:2001MAY17	657	725	forward 3	zf-C2H2	Zinc finger, C2H2 type	8.60E-07
195	LI:1174809.1:2001MAY17	431	499	forward 2	zf-C2H2	Zinc finger, C2H2 type	1.20E-04
196	LI:1175131.1:2001MAY17	185	307	forward 2	KRAB	KRAB box	6.80E-26
196	LI:1175131.1:2001MAY17	842	910	forward 2	zf-C2H2	Zinc finger, C2H2 type	3.60E-07
197	LI:1188801.10:2001MAY17	724	966	forward 1	PDZ	PDZ domain (Also known as DHR or GLGF).	1.30E-16
198	LI:1189176.27:2001MAY17	509	577	forward 2	MORN	MORN repeat	1.20E-05
199	LI:197739.4:2001MAY17	171	293	forward 3	KRAB	KRAB box	1.20E-23
199	LI:197739.4:2001MAY17	768	836	forward 3	zf-C2H2	Zinc finger, C2H2 type	2.50E-06
200	LI:2049016.1:2001MAY17	200	322	forward 2	KRAB	KRAB box	1.20E-27
201	LI:2049137.1:2001MAY17	260	382	forward 2	KRAB	KRAB box	5.90E-22
201	LI:2049137.1:2001MAY17	875	943	forward 2	zf-C2H2	Zinc finger, C2H2 type	1.90E-06
202	LI:2051907.1:2001MAY17	117	203	forward 3	efhand	EF hand	2.10E-04
202	LI:2051907.1:2001MAY17	912	1187	forward 3	mito_carr	Mitochondrial carrier protein	1.70E-32
203	LI:2117996.13:2001MAY17	717	1028	forward 3	GAT	GAT domain	2.70E-36
203	LI:2117996.13:2001MAY17	84	515	forward 3	VHS	VHS domain	2.90E-67
204	LI:2118683.15:2001MAY17	427	774	forward 1	PH	PH domain	1.20E-10
204	LI:2118683.15:2001MAY17	1069	1527	forward 1	RhoGAP	RhoGAP domain	6.20E-57
204	LI:2118683.15:2001MAY17	241	330	forward 1	WW	WW domain	4.30E-04
205	LI:2120312.1:2001MAY17	951	1262	forward 3	Ribosomal_L7Ae	Ribosomal protein L7Ae/L30e/S12e/Gadd45 family	1.90E-16
206	LI:2121328.17:2001MAY17	432	530	forward 3	ank	Ankyrin repeat	2.20E-06
207	LI:2121802.5:2001MAY17	188	310	forward 2	KRAB	KRAB box	1.20E-26
207	LI:2121802.5:2001MAY17	977	1045	forward 2	zf-C2H2	Zinc finger, C2H2 type	3.50E-06
208	LI:2123406.9:2001MAY17	406	612	forward 1	CUB	CUB domain	4.90E-05
208	LI:2123406.9:2001MAY17	226	396	forward 1	sushi	Sushi domain (SCR repeat)	3.50E-08
209	LI:216129.45:2001MAY17	1122	1361	forward 3	UBX	UBX domain	4.40E-04
210	LI:2186630.1:2001MAY17	135	257	forward 3	KRAB	KRAB box	1.10E-22
211	LI:2188206.2:2001MAY17	570	725	forward 3	Integrase	Integrase DNA binding domain	9.80E-20
212	LI:2199710.9:2001MAY17	657	1454	forward 3	DEAD	DEAD/DEAH box helicase	2.40E-49
212	LI:2199710.9:2001MAY17	1611	1802	forward 3	helicase_C	Helicase conserved C-terminal domain	4.50E-09

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
213	LI:2209335.2:2001MAY17	1056	1154	forward 3	ank	Ankyrin repeat	6.80E-06
214	LI:230980.13:2001MAY17	64	162	forward 1	ank	Ankyrin repeat	4.50E-10
215	LI:244421.37:2001MAY17	3	101	forward 3	zf-CXXC	CXXC zinc finger	6.10E-06
216	LI:341998.1:2001MAY17	308	598	forward 2	CH	Calponin homology (CH) domain	4.40E-13
217	LI:347931.10:2001MAY17	905	1177	forward 2	PH	PH domain	1.30E-04
218	LI:350771.42:2001MAY17	793	1083	forward 1	Alpha_adaptin_C	Alpha adaptin AP2, C-terminal domain	3.30E-68
219	LI:354423.6:2001MAY17	855	1166	forward 3	BTB	BTB/POZ domain	8.60E-24
220	LI:399333.8:2001MAY17	1235	2398	forward 2	RNB	RNB-like protein	9.90E-100
221	LI:445084.36:2001MAY17	105	551	forward 3	DUF101	Protein of unknown function DUF101	3.70E-12
222	LI:454087.3:2001MAY17	181	303	forward 1	KRAB	KRAB box	3.30E-25
222	LI:454087.3:2001MAY17	754	822	forward 1	zf-C2H2	Zinc finger, C2H2 type	1.80E-06
223	LI:474887.1:2001MAY17	2795	3166	forward 2	UQ_con	Ubiquitin-conjugating enzyme	9.70E-19
224	LI:745251.1:2001MAY17	208	531	forward 1	BTB	BTB/POZ domain	2.40E-30
225	LI:747717.9:2001MAY17	937	1113	forward 1	lg	Immunoglobulin domain	1.50E-07
226	LI:806211.3:2001MAY17	876	944	forward 3	zf-C2H2	Zinc finger, C2H2 type	4.00E-06
227	LI:815072.1:2001MAY17	1	360	forward 1	Ribosomal_L10e	Ribosomal L10	1.10E-07
228	LI:817052.8:2001MAY17	1084	1206	forward 1	KRAB	KRAB box	9.50E-20
228	LI:817052.8:2001MAY17	2311	2379	forward 1	zf-C2H2	Zinc finger, C2H2 type	8.20E-08
229	LI:903392.45:2001MAY17	3	194	forward 3	K_tetra	K+ channel tetramerisation domain	1.60E-04
230	LI:013724.1:2001MAY17	20	1033	forward 2	V-ATPase_C	V-ATPase subunit C	7.50E-122
231	LI:191726.16:2001MAY17	1360	1716	forward 1	2OG-Fell_Oxy	2OG-Fe(II) oxygenase superfamily	5.20E-04
232	LI:202270.2:2001MAY17	1500	1829	forward 3	Yippee	Yippee putative zinc-binding protein	8.30E-68
233	LI:2119352.6:2001MAY17	358	753	forward 1	2OG-Fell_Oxy	2OG-Fe(II) oxygenase superfamily	4.10E-08
234	LI:2207776.11:2001MAY17	592	942	forward 1	ABC1	ABC1 family	2.50E-45
235	LI:256442.1:2001MAY17	1466	1717	forward 2	BAF	Barrier to autointegration factor	2.90E-30
235	LI:256442.1:2001MAY17	1473	1718	forward 3	BAF	Barrier to autointegration factor	3.10E-11
236	LI:330497.7:2001MAY17	61	312	forward 1	PAAD_DAPIN	PAAD/DAPIN/Pyrim domain	4.90E-05
237	LI:018494.1:2001MAY17	1	1200	forward 1	SSF	Sodium:solute symporter family	3.30E-08
238	LI:023518.2:2001MAY17	195	845	forward 3	vATP-synt_AC39	ATP synthase (C/AC39) subunit	1.20E-40
239	LI:053488.46:2001MAY17	1174	1410	forward 1	PDGF	Platelet-derived growth factor (PDGF)	1.80E-51
240	LI:058298.27:2001MAY17	665	1231	forward 2	pkinase	Protein kinase domain	3.30E-35
241	LI:1110046.1:2001MAY17	84	830	forward 3	MIP	Major intrinsic protein	2.60E-56

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
242	LI:1166752.11:2001MAY17	174	296	forward 3	KRAB	KRAB box	1.20E-22
242	LI:1166752.11:2001MAY17	897	965	forward 3	zf-C2H2	Zinc finger, C2H2 type	1.70E-07
243	LI:1173766.1:2001MAY17	289	411	forward 1	KRAB	KRAB box	5.50E-27
243	LI:1173766.1:2001MAY17	2008	2076	forward 1	zf-C2H2	Zinc finger, C2H2 type	1.70E-07
244	LI:1177952.4:2001MAY17	1257	2003	forward 3	Band_7	SPFH domain / Band 7 family	2.00E-22
244	LI:1177952.4:2001MAY17	257	325	forward 2	zf-C2H2	Zinc finger, C2H2 type	1.50E-06
245	LI:1178064.3:2001MAY17	274	396	forward 1	KRAB	KRAB box	3.80E-10
245	LI:1178064.3:2001MAY17	2194	2262	forward 1	zf-C2H2	Zinc finger, C2H2 type	2.20E-06
246	LI:1183121.1:2001MAY17	1080	1148	forward 3	zf-C2H2	Zinc finger, C2H2 type	6.70E-07
247	LI:1190431.13:2001MAY17	1873	2073	forward 1	sushi	Sushi domain (SCR repeat)	7.20E-21
248	LI:199121.14:2001MAY17	1347	1577	forward 3	disintegrin	Disintegrin	2.70E-21
248	LI:199121.14:2001MAY17	318	668	forward 3	Pep_M12B_propep	Reprolysin family propeptide	8.00E-57
248	LI:199121.14:2001MAY17	714	1298	forward 3	Reprolysin	Reprolysin (M12B) family zinc metalloprotease	4.50E-107
249	LI:202630.5:2001MAY17	986	1726	forward 2	7tm_1	7 transmembrane receptor (rhodopsin family)	1.40E-30
250	LI:2034488.1:2001MAY17	278	346	forward 2	zf-C2H2	Zinc finger, C2H2 type	2.70E-04
251	LI:2051434.8:2001MAY17	847	1599	forward 1	carb_anhydrase	Eukaryotic-type carbonic anhydrase	2.40E-169
251	LI:2051434.8:2001MAY17	60	830	forward 3	carb_anhydrase	Eukaryotic-type carbonic anhydrase	3.80E-139
252	LI:2118475.9:2001MAY17	712	957	forward 1	UPAR_LY6	u-PAR/Ly-6 domain	2.30E-32
253	LI:218849.24:2001MAY17	482	1669	forward 2	OATP_C	Organic Anion Transporter Polypeptide (OATP) family, C-terminus	8.60E-215
253	LI:218849.24:2001MAY17	1898	2380	forward 2	OATP_N	Organic Anion Transporter Polypeptide (OATP) family, N-terminus	1.00E-67
254	LI:2199824.5:2001MAY17	480	1151	forward 3	Tropomyosin	Tropomyosin	1.50E-58
254	LI:2199824.5:2001MAY17	458	1189	forward 2	Tropomyosin	Tropomyosin	6.20E-08
255	LI:233018.32:2001MAY17	119	334	forward 2	crystall	Beta/Gamma crystallin	5.70E-11
255	LI:233018.32:2001MAY17	1016	1144	forward 2	Richn_B_lectin	QXW lectin repeat	5.20E-08
256	LI:236295.8:2001MAY17	439	741	forward 1	IRF	Interferon regulatory factor transcription factor	5.00E-20
257	LI:286989.14:2001MAY17	325	807	forward 1	MH1	MH1 domain	6.30E-68
257	LI:286989.14:2001MAY17	1093	1626	forward 1	MH2	MH2 domain	8.40E-123
258	LI:345320.4:2001MAY17	665	733	forward 2	zf-C2H2	Zinc finger, C2H2 type	1.80E-06
259	LI:355693.18:2001MAY17	2221	2373	forward 1	PSI	Plexin repeat	2.20E-17
259	LI:355693.18:2001MAY17	841	2166	forward 1	Sema	Sema domain	1.10E-125

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
259	U:355693.18:2001MAY17	3553	3807	forward 1	TIG	IPT/TIG domain	2.10E-23
260	U:359876.1:2001MAY17	599	1345	forward 2	7tm_1	7 transmembrane receptor (rhodopsin family)	1.20E-28
261	U:406664.32:2001MAY17	463	639	forward 1	SRF-TF	SRF-type transcription factor (DNA-binding and dimerisation domain)	2.10E-37
262	U:410324.1:2001MAY17	1655	1930	forward 2	cadherin	Cadherin domain	2.30E-19
263	U:414376.12:2001MAY17	1637	2224	forward 2	lon_trans	lon transport protein	6.60E-44
263	U:414376.12:2001MAY17	976	1272	forward 1	K_tetra	K+ channel tetramerisation domain	2.40E-46
264	U:452089.1:2001MAY17	107	268	forward 2	Ribosomal_L5	Ribosomal protein L5	6.10E-26
264	U:452089.1:2001MAY17	278	577	forward 2	Ribosomal_L5_C	ribosomal L5P family C-terminus	2.50E-60
265	U:481614.43:2001MAY17	614	1594	forward 2	pkkinase	Protein kinase domain	3.70E-13
265	U:481614.43:2001MAY17	798	1418	forward 3	pkkinase	Protein kinase domain	2.20E-08
266	U:809605.2:2001MAY17	1935	2003	forward 3	zf-C2H2	Zinc finger, C2H2 type	3.60E-05
267	U:816437.25:2001MAY17	1753	2580	forward 1	lig_chan	Ligand-gated ion channel	5.50E-110
268	U:817827.5:2001MAY17	329	538	forward 2	elf-5a	Eukaryotic initiation factor 5A hypusine, DNA-binding OB fold	3.40E-36
268	U:817827.5:2001MAY17	101	325	forward 2	elf-5a_N	Eukaryotic initiation factor 5A hypusine, SH3-like barrel domain	2.30E-50
269	U:002345.15:2001MAY17	261	527	forward 3	ACBP	Acyl CoA binding protein	4.40E-56
270	U:022629.5:2001MAY17	281	430	forward 2	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	4.90E-05
271	U:061031.4:2001MAY17	20	715	forward 2	lon_trans	lon transport protein	4.50E-18
272	U:108232.2:2001MAY17	146	769	forward 2	TatD_DNase	TatD related DNase	5.20E-08
273	U:1085493.16:2001MAY17	10	816	forward 1	A_deaminase	Adenosine/AMP deaminase	9.40E-13
274	U:1085513.2:2001MAY17	537	1742	forward 3	Na_H_Exchanger	Sodium/hydrogen exchanger family	2.40E-18
275	U:1086797.9:2001MAY17	501	1790	forward 3	Sema	Sema domain	2.00E-176
276	U:1088446.1:2001MAY17	71	193	forward 2	KRAB	KRAB box	9.60E-24
276	U:1088446.1:2001MAY17	1659	1727	forward 3	zf-C2H2	Zinc finger, C2H2 type	7.40E-05
277	U:1133764.3:2001MAY17	383	706	forward 2	spectrin	Spectrin repeat	9.60E-11
278	U:1147614.5:2001MAY17	525	701	forward 3	lg	Immunoglobulin domain	1.70E-11
279	U:1181710.1:2001MAY17	86	154	forward 2	zf-C2H2	Zinc finger, C2H2 type	1.10E-05
280	U:1183192.1:2001MAY17	992	1060	forward 2	zf-C2H2	Zinc finger, C2H2 type	2.20E-06
281	U:1188786.15:2001MAY17	1320	1406	forward 3	efhand	EF hand	8.60E-06
282	U:145626.1:2001MAY17	637	804	forward 1	sushi	Sushi domain (SCR repeat)	5.20E-14

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
282	U:145626.1:2001MAY17	1328	1492	forward 2	sushi	Sushi domain (SCR repeat)	3.70E-04
283	U:147869.3:2001MAY17	4	1749	forward 1	Patched	Patched family	2.00E-07
284	U:151747.4:2001MAY17	103	207	forward 1	SAP	SAP domain	1.40E-07
284	U:151747.4:2001MAY17	1096	1254	forward 1	zf-MIZ	MIZ zinc finger	7.60E-35
285	U:198296.1:2001MAY17	646	783	forward 1	Kelch	Kelch motif	5.50E-14
286	U:200117.4:2001MAY17	670	771	forward 1	TPR	TPR Domain	8.60E-04
287	U:200704.1:2001MAY17	1311	1493	forward 3	Ig	Immunoglobulin domain	3.00E-06
288	U:2049995.3:2001MAY17	1516	2352	forward 1	pklnase	Protein kinase domain	1.90E-68
289	U:2052097.2:2001MAY17	504	605	forward 3	TPR	TPR Domain	1.80E-04
290	U:209351.22:2001MAY17	300	410	forward 3	WD40	WD domain, G-beta repeat	4.80E-13
291	U:2120481.1:2001MAY17	501	842	forward 3	CUB	CUB domain	7.10E-14
292	U:2121610.13:2001MAY17	81	803	forward 3	7tm_1	7 transmembrane receptor (rhodopsin family)	7.70E-19
293	U:2191585.1:2001MAY17	424	846	forward 1	Steroid_dh	3-oxo-5-alpha-steroid 4-dehydrogenase	2.90E-39
293	U:2191585.1:2001MAY17	513	878	forward 3	Steroid_dh	3-oxo-5-alpha-steroid 4-dehydrogenase	3.80E-05
294	U:2198562.3:2001MAY17	1263	1688	forward 3	2-Hacid_DH_C	D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain	5.90E-08
295	U:2209684.5:2001MAY17	257	544	forward 2	SCAN	SCAN domain	4.50E-73
295	U:2209684.5:2001MAY17	1628	1696	forward 2	zf-C2H2	Zinc finger, C2H2 type	4.50E-07
296	U:222795.28:2001MAY17	1300	1587	forward 1	PH	PH domain	8.10E-20
297	U:228273.25:2001MAY17	404	625	forward 2	mbt	mbt repeat	6.60E-45
297	U:228273.25:2001MAY17	1400	1594	forward 2	SAM	SAM domain (Sterile alpha motif)	7.70E-08
297	U:228273.25:2001MAY17	1007	1102	forward 2	zf-C2HC	Zinc finger, C2HC type	3.40E-11
298	U:232386.31:2001MAY17	1395	1499	forward 3	zf-MYND	MYND finger	6.90E-07
299	U:233089.2:2001MAY17	309	389	forward 3	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type (and similar).	5.70E-04
300	U:240641.10:2001MAY17	785	883	forward 2	ank	Ankyrin repeat	4.80E-09
301	U:243871.4:2001MAY17	722	1006	forward 2	Ribosomal_L7Ae	Ribosomal protein L7Ae/L30e/S12e/Gadd45 family	4.20E-31
302	U:245597.7:2001MAY17	319	555	forward 1	Ets	Ets-domain	8.40E-56
303	U:256009.31:2001MAY17	826	1380	forward 1	arf	ADP-ribosylation factor family	1.10E-54
303	U:256009.31:2001MAY17	311	697	forward 2	arf	ADP-ribosylation factor family	4.20E-05
304	U:262221.1:2001MAY17	306	731	forward 3	BTB	BTB/POZ domain	8.00E-16
305	U:332957.8:2001MAY17	579	722	forward 3	Kelch	Kelch motif	1.00E-08

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
306	LI:335352.13:2001MAY17	197	844	forward 2	IF4E	Eukaryotic initiation factor 4E	1.70E-136
307	LI:343844.7:2001MAY17	330	401	forward 3	zf-C2H2	Zinc finger, C2H2 type	5.60E-05
308	LI:344528.1:2001MAY17	1618	1728	forward 1	zf-MYND	MYND finger	6.80E-15
309	LI:374578.27:2001MAY17	493	702	forward 1	rrm	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	2.70E-20
310	LI:381993.13:2001MAY17	1477	2013	forward 1	ABC_tran	ABC transporter	1.40E-44
310	LI:381993.13:2001MAY17	5160	5696	forward 3	ABC_tran	ABC transporter	1.40E-44
311	LI:400373.2:2001MAY17	354	446	forward 3	EGF	EGF-like domain	9.40E-05
311	LI:400373.2:2001MAY17	1123	1215	forward 1	EGF	EGF-like domain	4.20E-04
312	LI:400963.6:2001MAY17	882	980	forward 3	ank	Ankyrin repeat	3.20E-09
313	LI:404874.8:2001MAY17	962	1372	forward 2	PAZ	PAZ domain	4.30E-51
313	LI:404874.8:2001MAY17	1808	2713	forward 2	Piwi	Piwi domain	2.10E-147
314	LI:405158.18:2001MAY17	806	904	forward 2	ank	Ankyrin repeat	3.20E-07
314	LI:405158.18:2001MAY17	1580	1810	forward 2	IBR	IBR domain	3.30E-26
315	LI:405889.22:2001MAY17	821	919	forward 2	ank	Ankyrin repeat	5.70E-08
316	LI:411151.31:2001MAY17	1861	2031	forward 1	LIM	LIM domain	3.90E-14
316	LI:411151.31:2001MAY17	43	282	forward 1	PDZ	PDZ domain (Also known as DHR or GLGF).	1.50E-17
317	LI:411313.51:2001MAY17	1262	1438	forward 2	SH3	SH3 domain	1.10E-04
318	LI:417127.1:2001MAY17	361	483	forward 1	KRAB	KRAB box	2.90E-26
319	LI:429817.44:2001MAY17	303	476	forward 3	LIM	LIM domain	3.30E-19
320	LI:474134.23:2001MAY17	780	890	forward 3	ank	Ankyrin repeat	1.60E-06
321	LI:475378.3:2001MAY17	2426	2623	forward 2	FYVE	FYVE zinc finger	1.50E-15
321	LI:475378.3:2001MAY17	2057	2338	forward 2	PH	PH domain	4.40E-13
321	LI:475378.3:2001MAY17	1403	1966	forward 2	RhoGEF	RhoGEF domain	2.40E-07
322	LI:749588.15:2001MAY17	2265	2924	forward 3	GP36	Env gp36 protein (HERV/MMTV type)	3.40E-16
322	LI:749588.15:2001MAY17	74	193	forward 2	Integrase_Zn	Integrase Zinc binding domain	4.10E-11
322	LI:749588.15:2001MAY17	224	697	forward 2	rve	Integrase core domain	1.70E-30
323	LI:757736.17:2001MAY17	367	465	forward 1	ank	Ankyrin repeat	3.00E-08
324	LI:817278.4:2001MAY17	92	307	forward 2	rrm	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	1.30E-22
325	LI:027320.5:2001MAY17	158	358	forward 2	SAM	SAM domain (Sterile alpha motif)	6.30E-06
326	LI:204635.5:2001MAY17	284	619	forward 2	Rieske	Rieske (2Fe-2S) domain	6.20E-07

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
327	LI:215532.38:2001MAY17	416	862	forward 2	PAP2	PAP2 superfamily	1.10E-04
328	LI:228319.6:2001MAY17	527	748	forward 2	mbf	mbf repeat	6.30E-39
329	LI:236589.24:2001MAY17	599	1885	forward 2	DUF254	SAND family protein	5.80E-270
330	LI:247444.3:2001MAY17	131	415	forward 2	TB2_DP1_HVA22	TB2/DP1, HVA22 family	9.90E-35
331	LI:332404.20:2001MAY17	1943	2179	forward 2	Cache	Cache domain	1.10E-04
332	LG:1088459.4:2001JUN22	422	490	forward 2	zf-C2H2	Zinc finger, C2H2 type	2.60E-07
333	LG:1501495.1:2001JUN22	109	231	forward 1	KRAB	KRAB box	1.20E-24
333	LG:1501495.1:2001JUN22	868	936	forward 1	zf-C2H2	Zinc finger, C2H2 type	2.80E-07
333	LG:1501495.1:2001JUN22	2067	2135	forward 3	zf-C2H2	Zinc finger, C2H2 type	4.10E-07
334	LG:334284.10:2001JUN22	1	756	forward 1	TTL	Tubulin-tyrosine ligase family	6.80E-16
335	LG:345279.19:2001JUN22	151	585	forward 1	pro_isomerase	Cyclophilin type peptidyl-prolyl cis-trans isomerase	2.00E-30
336	LG:7689681.1:2001JUN22	112	180	forward 1	zf-C2H2	Zinc finger, C2H2 type	1.00E-07
337	LG:7690093.1:2001JUN22	456	524	forward 3	zf-C2H2	Zinc finger, C2H2 type	4.80E-08
338	LG:7690175.3:2001JUN22	155	223	forward 2	zf-C2H2	Zinc finger, C2H2 type	2.90E-06
339	LG:7697128.1:2001JUN22	125	367	forward 2	lg	Immunoglobulin domain	5.00E-05
340	LG:006394.20:2001JUN22	643	1101	forward 1	RhoGAP	RhoGAP domain	6.20E-57
341	LG:1012069.1:2001JUN22	430	528	forward 1	ank	Ankyrin repeat	2.50E-06
342	LG:104533.11:2001JUN22	950	1183	forward 2	death	Death domain	2.10E-10
343	LG:1045853.23:2001JUN22	109	837	forward 1	Beach	Belge/BEACH domain	9.80E-17
344	LG:1081017.8:2001JUN22	443	541	forward 2	ank	Ankyrin repeat	6.20E-08
344	LG:1081017.8:2001JUN22	651	749	forward 3	ank	Ankyrin repeat	1.90E-06
345	LG:1090358.6:2001JUN22	663	779	forward 3	KRAB	KRAB box	1.60E-19
346	LG:1135312.7:2001JUN22	86	910	forward 2	aldo_ket_red	Aldo/keto reductase family	5.70E-38
346	LG:1135312.7:2001JUN22	154	957	forward 1	aldo_ket_red	Aldo/keto reductase family	4.00E-11
347	LG:1328501.2:2001JUN22	289	411	forward 1	KRAB	KRAB box	8.60E-26
347	LG:1328501.2:2001JUN22	934	1002	forward 1	zf-C2H2	Zinc finger, C2H2 type	3.10E-07
348	LG:133095.1:2001JUN22	1296	1364	forward 3	zf-C2H2	Zinc finger, C2H2 type	4.20E-06
349	LG:135379.5:2001JUN22	358	534	forward 1	wvc	von Willebrand factor type C domain	1.30E-09
350	LG:1365581.3:2001JUN22	154	276	forward 1	KRAB	KRAB box	2.70E-27
351	LG:1383156.20:2001JUN22	911	1411	forward 2	PSAP	Surfactant associated polypeptide	2.30E-105
352	LG:1501767.18:2001JUN22	666	734	forward 3	zf-C2H2	Zinc finger, C2H2 type	1.90E-05



TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
353	LG:1501890.8:2001JUN22	235	516	forward 1	FCH	Fes/CIP4 homology domain	7.60E-33
353	LG:1501890.8:2001JUN22	1876	2046	forward 1	SH3	SH3 domain	6.60E-13
354	LG:203434.23:2001JUN22	202	1080	forward 1	filament	Intermediate filament protein	1.50E-08
355	LG:204724.5:2001JUN22	1	390	forward 1	Adeno_E1B_19K	Adenovirus E1B 19K protein / small t-antigen	5.40E-40
355	LG:204724.5:2001JUN22	59	454	forward 2	Adeno_E1B_19K	Adenovirus E1B 19K protein / small t-antigen	5.00E-08
355	LG:204724.5:2001JUN22	600	1751	forward 3	Adeno_E1B_55K	Adenovirus E1B 55K protein / large t-antigen	4.80E-260
356	LG:257107.16:2001JUN22	594	890	forward 3	PH	PH domain	6.40E-21
357	LG:353530.4:2001JUN22	2197	2298	forward 1	TPR	TPR Domain	8.10E-04
358	LG:7683573.3:2001JUN22	289	411	forward 1	KRAB	KRAB box	8.20E-22
359	LG:7684224.1:2001JUN22	385	561	forward 1	LIM	LIM domain	9.60E-17
360	LG:7690365.2:2001JUN22	744	866	forward 3	KRAB	KRAB box	2.10E-22
360	LG:7690365.2:2001JUN22	1500	1568	forward 3	zf-C2H2	Zinc finger, C2H2 type	3.60E-05
361	LG:968691.1:2001JUN22	208	531	forward 1	BTB	BTB/POZ domain	2.40E-30
362	LG:983076.7:2001JUN22	1235	2398	forward 2	RNB	RNB-like protein	3.00E-100
363	LG:986291.1:2001JUN22	127	570	forward 1	Ribosomal_L18p	Ribosomal L18p/L5e family	4.10E-74
364	LG:990347.41:2001JUN22	1791	2132	forward 3	PH	PH domain	2.70E-17
365	LG:998305.4:2001JUN22	216	314	forward 3	ank	Ankyrin repeat	9.60E-07
366	LG:463420.16:2001JUN22	1873	2427	forward 1	Glyco_transf_25	Glycosyltransferase family 25 (LPS biosynthesis protein)	2.00E-72
366	LG:463420.16:2001JUN22	2460	2885	forward 3	Glyco_transf_25	Glycosyltransferase family 25 (LPS biosynthesis protein)	5.00E-19
367	LG:979059.3:2001JUN22	1186	2418	forward 1	DUF254	SAND family protein	2.60E-273
368	LG:1045509.22:2001JUN22	77	1252	forward 2	transmembrane4	Tetraspanin family	2.10E-07
369	LG:246935.4:2001JUN22	85	519	forward 1	Smg4_UPF3	Smg-4/UPF3 family	7.60E-58
370	LG:321069.2:2001JUN22	514	807	forward 1	mito_carr	Mitochondrial carrier protein	2.60E-30
371	LG:346724.14:2001JUN22	559	690	forward 1	LEM	LEM domain	1.00E-24
372	LG:411043.3:2001JUN22	272	1258	forward 2	adh_zinc	Zinc-binding dehydrogenase	1.00E-19
373	LG:978620.7:2001JUN22	903	998	forward 3	EGF	EGF-like domain	6.10E-06
373	LG:978620.7:2001JUN22	531	650	forward 3	ldl_recept_a	Low-density lipoprotein receptor domain class	2.30E-09
373	LG:978620.7:2001JUN22	87	506	forward 3	MAM	MAM domain	2.00E-07
374	LG:982784.1:2001JUN22	582	650	forward 3	zf-C2H2	Zinc finger, C2H2 type	2.90E-05
375	LG:007574.21:2001JUN22	1627	2214	forward 1	BAR	BAR domain	1.00E-05

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
375	LG:007574.21:2001JUN22	1109	1615	forward 2	RhoGEF	RhoGEF domain	5.80E-05
375	LG:007574.21:2001JUN22	3181	3357	forward 1	SH3	SH3 domain	9.50E-12
376	LG:013856.18:2001JUN22	276	368	forward 3	WW	WW domain	1.50E-04
377	LG:027320.7:2001JUN22	158	358	forward 2	SAM	SAM domain (Sterile alpha motif)	6.30E-06
378	LG:077967.9:2001JUN22	1249	2028	forward 1	pkinase	Protein kinase domain	1.10E-84
378	LG:077967.9:2001JUN22	640	870	forward 1	SH2	SH2 domain	3.20E-31
379	LG:128475.9:2001JUN22	252	362	forward 3	ank	Ankyrin repeat	1.60E-06
379	LG:128475.9:2001JUN22	25	123	forward 1	ank	Ankyrin repeat	1.80E-04
380	LG:1398104.15:2001JUN22	279	572	forward 3	K_tetra	K+ channel tetramerisation domain	2.80E-27
381	LG:1454018.10:2001JUN22	2505	2654	forward 3	KA1	Kinase associated domain 1	4.00E-21
381	LG:1454018.10:2001JUN22	477	1232	forward 3	pkinase	Protein kinase domain	3.80E-101
381	LG:1454018.10:2001JUN22	1290	1409	forward 3	UBA	UBA/TS-N domain	8.20E-05
382	LG:221548.14:2001JUN22	785	883	forward 2	ank	Ankyrin repeat	4.80E-09
383	LG:227500.5:2001JUN22	869	1042	forward 2	LIM	LIM domain	5.80E-11
384	LG:228273.22:2001JUN22	404	625	forward 2	mbt	mbt repeat	6.60E-45
384	LG:228273.22:2001JUN22	1400	1594	forward 2	SAM	SAM domain (Sterile alpha motif)	7.70E-08
384	LG:228273.22:2001JUN22	1007	1102	forward 2	zf-C2HC	Zinc finger, C2HC type	3.40E-11
385	LG:235432.1:2001JUN22	343	585	forward 1	SAND	SAND domain	3.50E-46
386	LG:236904.20:2001JUN22	537	824	forward 3	PH	PH domain	4.00E-21
387	LG:253193.21:2001JUN22	2297	2539	forward 2	mito_carr	Mitochondrial carrier protein	3.30E-07
388	LG:332161.3:2001JUN22	146	715	forward 2	ras	Ras family	2.70E-59
389	LG:332923.5:2001JUN22	2396	2665	forward 2	cadherin	Cadherin domain	1.00E-23
390	LG:343500.27:2001JUN22	411	695	forward 3	mito_carr	Mitochondrial carrier protein	1.70E-20
391	LG:369703.9:2001JUN22	112	1788	forward 1	Sec1	Sec1 family	8.00E-194
392	LG:415378.3:2001JUN22	160	552	forward 1	Reeler	Reeler domain	7.50E-77
392	LG:415378.3:2001JUN22	1885	2028	forward 1	tsp_1	Thrombospondin type 1 domain	3.10E-23
393	LG:458583.1:2001JUN22	31	141	forward 1	WD40	WD domain, G-beta repeat	4.60E-08
394	LG:7690373.1:2001JUN22	86	154	forward 2	zf-C2H2	Zinc finger, C2H2 type	1.10E-05
395	LG:898324.13:2001JUN22	184	294	forward 1	notch	Notch (DSL) domain	1.10E-04
396	LG:979167.5:2001JUN22	696	1064	forward 3	cyclin	Cyclin, N-terminal domain	3.80E-11

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
66	LG:1080918.1:2001MAR30	1	788	forward 1	TM	Non-Cytosolic
66	LG:1080918.1:2001MAR30	789	811	forward 1	TM	Transmembrane
66	LG:1080918.1:2001MAR30	812	818	forward 1	TM	Cytosolic
67	LG:1093747.15:2001MAR30	1	14	forward 1	TM	Non-Cytosolic
67	LG:1093747.15:2001MAR30	15	32	forward 1	TM	Transmembrane
67	LG:1093747.15:2001MAR30	33	43	forward 1	TM	Cytosolic
67	LG:1093747.15:2001MAR30	44	66	forward 1	TM	Transmembrane
67	LG:1093747.15:2001MAR30	67	831	forward 1	TM	Non-Cytosolic
67	LG:1093747.15:2001MAR30	1	9	forward 2	TM	Non-Cytosolic
67	LG:1093747.15:2001MAR30	10	32	forward 2	TM	Transmembrane
67	LG:1093747.15:2001MAR30	33	43	forward 2	TM	Cytosolic
67	LG:1093747.15:2001MAR30	44	66	forward 2	TM	Transmembrane
67	LG:1093747.15:2001MAR30	67	830	forward 2	TM	Non-Cytosolic
68	LG:1096896.47:2001MAR30	1	491	forward 2	TM	Non-Cytosolic
68	LG:1096896.47:2001MAR30	492	514	forward 2	TM	Transmembrane
68	LG:1096896.47:2001MAR30	515	625	forward 2	TM	Cytosolic
68	LG:1096896.47:2001MAR30	626	648	forward 2	TM	Transmembrane
68	LG:1096896.47:2001MAR30	649	657	forward 2	TM	Non-Cytosolic
68	LG:1096896.47:2001MAR30	658	680	forward 2	TM	Transmembrane
68	LG:1096896.47:2001MAR30	681	729	forward 2	TM	Cytosolic
68	LG:1096896.47:2001MAR30	730	752	forward 2	TM	Transmembrane
68	LG:1096896.47:2001MAR30	753	792	forward 2	TM	Non-Cytosolic
69	LG:1098931.39:2001MAR30	1	430	forward 3	TM	Non-Cytosolic
69	LG:1098931.39:2001MAR30	431	448	forward 3	TM	Transmembrane
69	LG:1098931.39:2001MAR30	449	541	forward 3	TM	Cytosolic
69	LG:1098931.39:2001MAR30	542	564	forward 3	TM	Transmembrane
69	LG:1098931.39:2001MAR30	565	3052	forward 3	TM	Non-Cytosolic
70	LG:1100823.1:2001MAR30	1	31	forward 1	TM	Cytosolic
70	LG:1100823.1:2001MAR30	32	54	forward 1	TM	Transmembrane
70	LG:1100823.1:2001MAR30	55	68	forward 1	TM	Non-Cytosolic
70	LG:1100823.1:2001MAR30	69	91	forward 1	TM	Transmembrane
70	LG:1100823.1:2001MAR30	92	280	forward 1	TM	Cytosolic
70	LG:1100823.1:2001MAR30	1	98	forward 2	TM	Cytosolic
70	LG:1100823.1:2001MAR30	99	121	forward 2	TM	Transmembrane
70	LG:1100823.1:2001MAR30	122	226	forward 2	TM	Non-Cytosolic
70	LG:1100823.1:2001MAR30	227	249	forward 2	TM	Transmembrane
70	LG:1100823.1:2001MAR30	250	255	forward 2	TM	Cytosolic
70	LG:1100823.1:2001MAR30	256	278	forward 2	TM	Transmembrane
70	LG:1100823.1:2001MAR30	279	279	forward 2	TM	Non-Cytosolic
71	LG:1166387.1:2001MAR30	1	700	forward 1	TM	Non-Cytosolic
71	LG:1166387.1:2001MAR30	701	723	forward 1	TM	Transmembrane
71	LG:1166387.1:2001MAR30	724	804	forward 1	TM	Cytosolic
71	LG:1166387.1:2001MAR30	1	607	forward 3	TM	Non-Cytosolic
71	LG:1166387.1:2001MAR30	608	630	forward 3	TM	Transmembrane
71	LG:1166387.1:2001MAR30	631	713	forward 3	TM	Cytosolic
71	LG:1166387.1:2001MAR30	714	736	forward 3	TM	Transmembrane
71	LG:1166387.1:2001MAR30	737	779	forward 3	TM	Non-Cytosolic
71	LG:1166387.1:2001MAR30	780	802	forward 3	TM	Transmembrane
71	LG:1166387.1:2001MAR30	803	804	forward 3	TM	Cytosolic
72	LG:1383036.49:2001MAR30	1	226	forward 1	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
72	LG:1383036.49:2001MAR30	227	249	forward 1	TM	Transmembrane
72	LG:1383036.49:2001MAR30	250	407	forward 1	TM	Cytosolic
72	LG:1383036.49:2001MAR30	408	430	forward 1	TM	Transmembrane
72	LG:1383036.49:2001MAR30	431	1130	forward 1	TM	Non-Cytosolic
72	LG:1383036.49:2001MAR30	1	719	forward 3	TM	Non-Cytosolic
72	LG:1383036.49:2001MAR30	720	742	forward 3	TM	Transmembrane
72	LG:1383036.49:2001MAR30	743	963	forward 3	TM	Cytosolic
72	LG:1383036.49:2001MAR30	964	986	forward 3	TM	Transmembrane
72	LG:1383036.49:2001MAR30	987	1129	forward 3	TM	Non-Cytosolic
73	LG:1452353.14:2001MAR30	1326	1391	forward 3	SP	
73	LG:1452353.14:2001MAR30	1	2943	forward 1	TM	Non-Cytosolic
73	LG:1452353.14:2001MAR30	2944	2966	forward 1	TM	Transmembrane
73	LG:1452353.14:2001MAR30	2967	2996	forward 1	TM	Cytosolic
73	LG:1452353.14:2001MAR30	2997	3019	forward 1	TM	Transmembrane
73	LG:1452353.14:2001MAR30	3020	3042	forward 1	TM	Non-Cytosolic
73	LG:1452353.14:2001MAR30	3043	3060	forward 1	TM	Transmembrane
73	LG:1452353.14:2001MAR30	3061	3157	forward 1	TM	Cytosolic
73	LG:1452353.14:2001MAR30	3158	3180	forward 1	TM	Transmembrane
73	LG:1452353.14:2001MAR30	3181	3580	forward 1	TM	Non-Cytosolic
73	LG:1452353.14:2001MAR30	3581	3603	forward 1	TM	Transmembrane
73	LG:1452353.14:2001MAR30	3604	3726	forward 1	TM	Cytosolic
73	LG:1452353.14:2001MAR30	3727	3749	forward 1	TM	Transmembrane
73	LG:1452353.14:2001MAR30	3750	3841	forward 1	TM	Non-Cytosolic
73	LG:1452353.14:2001MAR30	3842	3864	forward 1	TM	Transmembrane
73	LG:1452353.14:2001MAR30	3865	3884	forward 1	TM	Cytosolic
73	LG:1452353.14:2001MAR30	3885	3907	forward 1	TM	Transmembrane
73	LG:1452353.14:2001MAR30	3908	3916	forward 1	TM	Non-Cytosolic
73	LG:1452353.14:2001MAR30	3917	3935	forward 1	TM	Transmembrane
73	LG:1452353.14:2001MAR30	3936	3947	forward 1	TM	Cytosolic
73	LG:1452353.14:2001MAR30	3948	3967	forward 1	TM	Transmembrane
73	LG:1452353.14:2001MAR30	3968	3981	forward 1	TM	Non-Cytosolic
73	LG:1452353.14:2001MAR30	3982	4004	forward 1	TM	Transmembrane
73	LG:1452353.14:2001MAR30	4005	4144	forward 1	TM	Cytosolic
73	LG:1452353.14:2001MAR30	1	2903	forward 2	TM	Non-Cytosolic
73	LG:1452353.14:2001MAR30	2904	2926	forward 2	TM	Transmembrane
73	LG:1452353.14:2001MAR30	2927	2946	forward 2	TM	Cytosolic
73	LG:1452353.14:2001MAR30	2947	2969	forward 2	TM	Transmembrane
73	LG:1452353.14:2001MAR30	2970	3006	forward 2	TM	Non-Cytosolic
73	LG:1452353.14:2001MAR30	3007	3029	forward 2	TM	Transmembrane
73	LG:1452353.14:2001MAR30	3030	3112	forward 2	TM	Cytosolic
73	LG:1452353.14:2001MAR30	3113	3132	forward 2	TM	Transmembrane
73	LG:1452353.14:2001MAR30	3133	3141	forward 2	TM	Non-Cytosolic
73	LG:1452353.14:2001MAR30	3142	3164	forward 2	TM	Transmembrane
73	LG:1452353.14:2001MAR30	3165	3168	forward 2	TM	Cytosolic
73	LG:1452353.14:2001MAR30	3169	3191	forward 2	TM	Transmembrane
73	LG:1452353.14:2001MAR30	3192	3243	forward 2	TM	Non-Cytosolic
73	LG:1452353.14:2001MAR30	3244	3266	forward 2	TM	Transmembrane
73	LG:1452353.14:2001MAR30	3267	3300	forward 2	TM	Cytosolic
73	LG:1452353.14:2001MAR30	3301	3323	forward 2	TM	Transmembrane
73	LG:1452353.14:2001MAR30	3324	3579	forward 2	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
73	LG:1452353.14:2001MAR30	3580	3602	forward 2	TM	Transmembrane
73	LG:1452353.14:2001MAR30	3603	3846	forward 2	TM	Cytosolic
73	LG:1452353.14:2001MAR30	3847	3869	forward 2	TM	Transmembrane
73	LG:1452353.14:2001MAR30	3870	3915	forward 2	TM	Non-Cytosolic
73	LG:1452353.14:2001MAR30	3916	3935	forward 2	TM	Transmembrane
73	LG:1452353.14:2001MAR30	3936	4031	forward 2	TM	Cytosolic
73	LG:1452353.14:2001MAR30	4032	4054	forward 2	TM	Transmembrane
73	LG:1452353.14:2001MAR30	4055	4144	forward 2	TM	Non-Cytosolic
73	LG:1452353.14:2001MAR30	1	114	forward 3	TM	Non-Cytosolic
73	LG:1452353.14:2001MAR30	115	137	forward 3	TM	Transmembrane
73	LG:1452353.14:2001MAR30	138	202	forward 3	TM	Cytosolic
73	LG:1452353.14:2001MAR30	203	225	forward 3	TM	Transmembrane
73	LG:1452353.14:2001MAR30	226	234	forward 3	TM	Non-Cytosolic
73	LG:1452353.14:2001MAR30	235	257	forward 3	TM	Transmembrane
73	LG:1452353.14:2001MAR30	258	400	forward 3	TM	Cytosolic
73	LG:1452353.14:2001MAR30	401	423	forward 3	TM	Transmembrane
73	LG:1452353.14:2001MAR30	424	437	forward 3	TM	Non-Cytosolic
73	LG:1452353.14:2001MAR30	438	460	forward 3	TM	Transmembrane
73	LG:1452353.14:2001MAR30	461	617	forward 3	TM	Cytosolic
73	LG:1452353.14:2001MAR30	618	637	forward 3	TM	Transmembrane
73	LG:1452353.14:2001MAR30	638	1535	forward 3	TM	Non-Cytosolic
73	LG:1452353.14:2001MAR30	1536	1558	forward 3	TM	Transmembrane
73	LG:1452353.14:2001MAR30	1559	1638	forward 3	TM	Cytosolic
73	LG:1452353.14:2001MAR30	1639	1661	forward 3	TM	Transmembrane
73	LG:1452353.14:2001MAR30	1662	3140	forward 3	TM	Non-Cytosolic
73	LG:1452353.14:2001MAR30	3141	3163	forward 3	TM	Transmembrane
73	LG:1452353.14:2001MAR30	3164	3174	forward 3	TM	Cytosolic
73	LG:1452353.14:2001MAR30	3175	3197	forward 3	TM	Transmembrane
73	LG:1452353.14:2001MAR30	3198	3229	forward 3	TM	Non-Cytosolic
73	LG:1452353.14:2001MAR30	3230	3252	forward 3	TM	Transmembrane
73	LG:1452353.14:2001MAR30	3253	3291	forward 3	TM	Cytosolic
73	LG:1452353.14:2001MAR30	3292	3314	forward 3	TM	Transmembrane
73	LG:1452353.14:2001MAR30	3315	3415	forward 3	TM	Non-Cytosolic
73	LG:1452353.14:2001MAR30	3416	3438	forward 3	TM	Transmembrane
73	LG:1452353.14:2001MAR30	3439	3579	forward 3	TM	Cytosolic
73	LG:1452353.14:2001MAR30	3580	3602	forward 3	TM	Transmembrane
73	LG:1452353.14:2001MAR30	3603	4144	forward 3	TM	Non-Cytosolic
74	LG:1452435.15:2001MAR30	1	2028	forward 3	TM	Non-Cytosolic
74	LG:1452435.15:2001MAR30	2029	2051	forward 3	TM	Transmembrane
74	LG:1452435.15:2001MAR30	2052	2280	forward 3	TM	Cytosolic
75	LG:1498774.1:2001MAR30	1	224	forward 2	TM	Non-Cytosolic
75	LG:1498774.1:2001MAR30	225	247	forward 2	TM	Transmembrane
75	LG:1498774.1:2001MAR30	248	251	forward 2	TM	Cytosolic
76	LG:197180.1:2001MAR30	1	1282	forward 1	TM	Non-Cytosolic
76	LG:197180.1:2001MAR30	1283	1305	forward 1	TM	Transmembrane
76	LG:197180.1:2001MAR30	1306	1311	forward 1	TM	Cytosolic
76	LG:197180.1:2001MAR30	1312	1334	forward 1	TM	Transmembrane
76	LG:197180.1:2001MAR30	1335	1372	forward 1	TM	Non-Cytosolic
76	LG:197180.1:2001MAR30	1	707	forward 3	TM	Non-Cytosolic
76	LG:197180.1:2001MAR30	708	730	forward 3	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
76	LG:197180.1:2001MAR30	731	736	forward 3	TM	Cytosolic
76	LG:197180.1:2001MAR30	737	759	forward 3	TM	Transmembrane
76	LG:197180.1:2001MAR30	760	1304	forward 3	TM	Non-Cytosolic
76	LG:197180.1:2001MAR30	1305	1327	forward 3	TM	Transmembrane
76	LG:197180.1:2001MAR30	1328	1338	forward 3	TM	Cytosolic
76	LG:197180.1:2001MAR30	1339	1361	forward 3	TM	Transmembrane
76	LG:197180.1:2001MAR30	1362	1371	forward 3	TM	Non-Cytosolic
77	LG:199489.1:2001MAR30	1	1505	forward 1	TM	Non-Cytosolic
77	LG:199489.1:2001MAR30	1506	1528	forward 1	TM	Transmembrane
77	LG:199489.1:2001MAR30	1529	1534	forward 1	TM	Cytosolic
77	LG:199489.1:2001MAR30	1535	1552	forward 1	TM	Transmembrane
77	LG:199489.1:2001MAR30	1553	1566	forward 1	TM	Non-Cytosolic
77	LG:199489.1:2001MAR30	1567	1589	forward 1	TM	Transmembrane
77	LG:199489.1:2001MAR30	1590	1595	forward 1	TM	Cytosolic
77	LG:199489.1:2001MAR30	1596	1618	forward 1	TM	Transmembrane
77	LG:199489.1:2001MAR30	1619	1627	forward 1	TM	Non-Cytosolic
77	LG:199489.1:2001MAR30	1628	1650	forward 1	TM	Transmembrane
77	LG:199489.1:2001MAR30	1651	1656	forward 1	TM	Cytosolic
77	LG:199489.1:2001MAR30	1657	1679	forward 1	TM	Transmembrane
77	LG:199489.1:2001MAR30	1680	1898	forward 1	TM	Non-Cytosolic
77	LG:199489.1:2001MAR30	1	94	forward 2	TM	Cytosolic
77	LG:199489.1:2001MAR30	95	113	forward 2	TM	Transmembrane
77	LG:199489.1:2001MAR30	114	122	forward 2	TM	Non-Cytosolic
77	LG:199489.1:2001MAR30	123	142	forward 2	TM	Transmembrane
77	LG:199489.1:2001MAR30	143	154	forward 2	TM	Cytosolic
77	LG:199489.1:2001MAR30	155	177	forward 2	TM	Transmembrane
77	LG:199489.1:2001MAR30	178	217	forward 2	TM	Non-Cytosolic
77	LG:199489.1:2001MAR30	218	240	forward 2	TM	Transmembrane
77	LG:199489.1:2001MAR30	241	244	forward 2	TM	Cytosolic
77	LG:199489.1:2001MAR30	245	267	forward 2	TM	Transmembrane
77	LG:199489.1:2001MAR30	268	304	forward 2	TM	Non-Cytosolic
77	LG:199489.1:2001MAR30	305	327	forward 2	TM	Transmembrane
77	LG:199489.1:2001MAR30	328	347	forward 2	TM	Cytosolic
77	LG:199489.1:2001MAR30	348	370	forward 2	TM	Transmembrane
77	LG:199489.1:2001MAR30	371	394	forward 2	TM	Non-Cytosolic
77	LG:199489.1:2001MAR30	395	414	forward 2	TM	Transmembrane
77	LG:199489.1:2001MAR30	415	443	forward 2	TM	Cytosolic
77	LG:199489.1:2001MAR30	444	461	forward 2	TM	Transmembrane
77	LG:199489.1:2001MAR30	462	465	forward 2	TM	Non-Cytosolic
77	LG:199489.1:2001MAR30	466	488	forward 2	TM	Transmembrane
77	LG:199489.1:2001MAR30	489	548	forward 2	TM	Cytosolic
77	LG:199489.1:2001MAR30	549	571	forward 2	TM	Transmembrane
77	LG:199489.1:2001MAR30	572	580	forward 2	TM	Non-Cytosolic
77	LG:199489.1:2001MAR30	581	600	forward 2	TM	Transmembrane
77	LG:199489.1:2001MAR30	601	611	forward 2	TM	Cytosolic
77	LG:199489.1:2001MAR30	612	634	forward 2	TM	Transmembrane
77	LG:199489.1:2001MAR30	635	638	forward 2	TM	Non-Cytosolic
77	LG:199489.1:2001MAR30	639	658	forward 2	TM	Transmembrane
77	LG:199489.1:2001MAR30	659	738	forward 2	TM	Cytosolic
77	LG:199489.1:2001MAR30	739	761	forward 2	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
77	LG:199489.1:2001MAR30	762	790	forward 2	TM	Non-Cytosolic
77	LG:199489.1:2001MAR30	791	808	forward 2	TM	Transmembrane
77	LG:199489.1:2001MAR30	809	814	forward 2	TM	Cytosolic
77	LG:199489.1:2001MAR30	815	837	forward 2	TM	Transmembrane
77	LG:199489.1:2001MAR30	838	1065	forward 2	TM	Non-Cytosolic
77	LG:199489.1:2001MAR30	1066	1088	forward 2	TM	Transmembrane
77	LG:199489.1:2001MAR30	1089	1231	forward 2	TM	Cytosolic
77	LG:199489.1:2001MAR30	1232	1254	forward 2	TM	Transmembrane
77	LG:199489.1:2001MAR30	1255	1517	forward 2	TM	Non-Cytosolic
77	LG:199489.1:2001MAR30	1518	1540	forward 2	TM	Transmembrane
77	LG:199489.1:2001MAR30	1541	1624	forward 2	TM	Cytosolic
77	LG:199489.1:2001MAR30	1625	1647	forward 2	TM	Transmembrane
77	LG:199489.1:2001MAR30	1648	1656	forward 2	TM	Non-Cytosolic
77	LG:199489.1:2001MAR30	1657	1679	forward 2	TM	Transmembrane
77	LG:199489.1:2001MAR30	1680	1897	forward 2	TM	Cytosolic
77	LG:199489.1:2001MAR30	1	643	forward 3	TM	Non-Cytosolic
77	LG:199489.1:2001MAR30	644	666	forward 3	TM	Transmembrane
77	LG:199489.1:2001MAR30	667	738	forward 3	TM	Cytosolic
77	LG:199489.1:2001MAR30	739	761	forward 3	TM	Transmembrane
77	LG:199489.1:2001MAR30	762	800	forward 3	TM	Non-Cytosolic
77	LG:199489.1:2001MAR30	801	823	forward 3	TM	Transmembrane
77	LG:199489.1:2001MAR30	824	1230	forward 3	TM	Cytosolic
77	LG:199489.1:2001MAR30	1231	1253	forward 3	TM	Transmembrane
77	LG:199489.1:2001MAR30	1254	1507	forward 3	TM	Non-Cytosolic
77	LG:199489.1:2001MAR30	1508	1530	forward 3	TM	Transmembrane
77	LG:199489.1:2001MAR30	1531	1561	forward 3	TM	Cytosolic
77	LG:199489.1:2001MAR30	1562	1579	forward 3	TM	Transmembrane
77	LG:199489.1:2001MAR30	1580	1583	forward 3	TM	Non-Cytosolic
77	LG:199489.1:2001MAR30	1584	1606	forward 3	TM	Transmembrane
77	LG:199489.1:2001MAR30	1607	1655	forward 3	TM	Cytosolic
77	LG:199489.1:2001MAR30	1656	1678	forward 3	TM	Transmembrane
77	LG:199489.1:2001MAR30	1679	1897	forward 3	TM	Non-Cytosolic
78	LG:201908.3:2001MAR30	1	1139	forward 3	TM	Non-Cytosolic
78	LG:201908.3:2001MAR30	1140	1162	forward 3	TM	Transmembrane
78	LG:201908.3:2001MAR30	1163	1532	forward 3	TM	Cytosolic
79	LG:247245.26:2001MAR30	1	741	forward 2	TM	Non-Cytosolic
79	LG:247245.26:2001MAR30	742	764	forward 2	TM	Transmembrane
79	LG:247245.26:2001MAR30	765	825	forward 2	TM	Cytosolic
79	LG:247245.26:2001MAR30	1	774	forward 3	TM	Non-Cytosolic
79	LG:247245.26:2001MAR30	775	797	forward 3	TM	Transmembrane
79	LG:247245.26:2001MAR30	798	801	forward 3	TM	Cytosolic
79	LG:247245.26:2001MAR30	802	824	forward 3	TM	Transmembrane
79	LG:247245.26:2001MAR30	825	825	forward 3	TM	Non-Cytosolic
80	LG:256365.2:2001MAR30	1	27	forward 2	TM	Cytosolic
80	LG:256365.2:2001MAR30	28	45	forward 2	TM	Transmembrane
80	LG:256365.2:2001MAR30	46	795	forward 2	TM	Non-Cytosolic
81	LG:332923.4:2001MAR30	1	36	forward 1	TM	Cytosolic
81	LG:332923.4:2001MAR30	37	59	forward 1	TM	Transmembrane
81	LG:332923.4:2001MAR30	60	602	forward 1	TM	Non-Cytosolic
81	LG:332923.4:2001MAR30	603	625	forward 1	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
81	LG:332923.4:2001MAR30	626	645	forward 1	TM	Cytosolic
81	LG:332923.4:2001MAR30	646	664	forward 1	TM	Transmembrane
81	LG:332923.4:2001MAR30	665	1438	forward 1	TM	Non-Cytosolic
81	LG:332923.4:2001MAR30	1	852	forward 3	TM	Non-Cytosolic
81	LG:332923.4:2001MAR30	853	875	forward 3	TM	Transmembrane
81	LG:332923.4:2001MAR30	876	1187	forward 3	TM	Cytosolic
81	LG:332923.4:2001MAR30	1188	1210	forward 3	TM	Transmembrane
81	LG:332923.4:2001MAR30	1211	1234	forward 3	TM	Non-Cytosolic
81	LG:332923.4:2001MAR30	1235	1257	forward 3	TM	Transmembrane
81	LG:332923.4:2001MAR30	1258	1437	forward 3	TM	Cytosolic
82	LG:335276.1:2001MAR30	1	493	forward 1	TM	Non-Cytosolic
82	LG:335276.1:2001MAR30	494	516	forward 1	TM	Transmembrane
82	LG:335276.1:2001MAR30	517	613	forward 1	TM	Cytosolic
82	LG:335276.1:2001MAR30	614	636	forward 1	TM	Transmembrane
82	LG:335276.1:2001MAR30	637	739	forward 1	TM	Non-Cytosolic
82	LG:335276.1:2001MAR30	740	762	forward 1	TM	Transmembrane
82	LG:335276.1:2001MAR30	763	802	forward 1	TM	Cytosolic
82	LG:335276.1:2001MAR30	803	825	forward 1	TM	Transmembrane
82	LG:335276.1:2001MAR30	826	845	forward 1	TM	Non-Cytosolic
83	LG:350272.2:2001MAR30	1	529	forward 1	TM	Non-Cytosolic
83	LG:350272.2:2001MAR30	530	552	forward 1	TM	Transmembrane
83	LG:350272.2:2001MAR30	553	559	forward 1	TM	Cytosolic
84	LG:350921.2:2001MAR30	1	566	forward 1	TM	Non-Cytosolic
84	LG:350921.2:2001MAR30	567	589	forward 1	TM	Transmembrane
84	LG:350921.2:2001MAR30	590	685	forward 1	TM	Cytosolic
84	LG:350921.2:2001MAR30	686	708	forward 1	TM	Transmembrane
84	LG:350921.2:2001MAR30	709	711	forward 1	TM	Non-Cytosolic
84	LG:350921.2:2001MAR30	712	734	forward 1	TM	Transmembrane
84	LG:350921.2:2001MAR30	735	831	forward 1	TM	Cytosolic
84	LG:350921.2:2001MAR30	1	550	forward 2	TM	Non-Cytosolic
84	LG:350921.2:2001MAR30	551	573	forward 2	TM	Transmembrane
84	LG:350921.2:2001MAR30	574	673	forward 2	TM	Cytosolic
84	LG:350921.2:2001MAR30	674	693	forward 2	TM	Transmembrane
84	LG:350921.2:2001MAR30	694	702	forward 2	TM	Non-Cytosolic
84	LG:350921.2:2001MAR30	703	725	forward 2	TM	Transmembrane
84	LG:350921.2:2001MAR30	726	830	forward 2	TM	Cytosolic
85	LG:406568.1:2001MAR30	1	618	forward 2	TM	Non-Cytosolic
85	LG:406568.1:2001MAR30	619	636	forward 2	TM	Transmembrane
85	LG:406568.1:2001MAR30	637	656	forward 2	TM	Cytosolic
85	LG:406568.1:2001MAR30	657	679	forward 2	TM	Transmembrane
85	LG:406568.1:2001MAR30	680	693	forward 2	TM	Non-Cytosolic
85	LG:406568.1:2001MAR30	694	716	forward 2	TM	Transmembrane
85	LG:406568.1:2001MAR30	717	770	forward 2	TM	Cytosolic
86	LG:411043.3:2001MAR30	1	99	forward 1	TM	Cytosolic
86	LG:411043.3:2001MAR30	100	122	forward 1	TM	Transmembrane
86	LG:411043.3:2001MAR30	123	181	forward 1	TM	Non-Cytosolic
86	LG:411043.3:2001MAR30	182	201	forward 1	TM	Transmembrane
86	LG:411043.3:2001MAR30	202	436	forward 1	TM	Cytosolic
86	LG:411043.3:2001MAR30	437	459	forward 1	TM	Transmembrane
86	LG:411043.3:2001MAR30	460	685	forward 1	TM	Non-Cytosolic



TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
87	LG:414376.20:2001MAR30	1	464	forward 2	TM	Non-Cytosolic
87	LG:414376.20:2001MAR30	465	487	forward 2	TM	Transmembrane
87	LG:414376.20:2001MAR30	488	542	forward 2	TM	Cytosolic
87	LG:414376.20:2001MAR30	543	565	forward 2	TM	Transmembrane
87	LG:414376.20:2001MAR30	566	579	forward 2	TM	Non-Cytosolic
87	LG:414376.20:2001MAR30	580	602	forward 2	TM	Transmembrane
87	LG:414376.20:2001MAR30	603	664	forward 2	TM	Cytosolic
87	LG:414376.20:2001MAR30	665	687	forward 2	TM	Transmembrane
87	LG:414376.20:2001MAR30	688	701	forward 2	TM	Non-Cytosolic
87	LG:414376.20:2001MAR30	702	720	forward 2	TM	Transmembrane
87	LG:414376.20:2001MAR30	721	726	forward 2	TM	Cytosolic
87	LG:414376.20:2001MAR30	727	749	forward 2	TM	Transmembrane
87	LG:414376.20:2001MAR30	750	2000	forward 2	TM	Non-Cytosolic
88	LG:457695.1:2001MAR30	1	257	forward 1	TM	Non-Cytosolic
88	LG:457695.1:2001MAR30	258	280	forward 1	TM	Transmembrane
88	LG:457695.1:2001MAR30	281	282	forward 1	TM	Cytosolic
89	LG:902390.2:2001MAR30	1	178	forward 1	TM	Cytosolic
89	LG:902390.2:2001MAR30	1	178	forward 3	TM	Cytosolic
90	LG:903565.20:2001MAR30	1	1239	forward 2	TM	Non-Cytosolic
90	LG:903565.20:2001MAR30	1240	1262	forward 2	TM	Transmembrane
90	LG:903565.20:2001MAR30	1263	1278	forward 2	TM	Cytosolic
90	LG:903565.20:2001MAR30	1279	1301	forward 2	TM	Transmembrane
90	LG:903565.20:2001MAR30	1302	1345	forward 2	TM	Non-Cytosolic
91	LG:978182.4:2001MAR30	1	819	forward 1	TM	Non-Cytosolic
91	LG:978182.4:2001MAR30	820	842	forward 1	TM	Transmembrane
91	LG:978182.4:2001MAR30	843	877	forward 1	TM	Cytosolic
91	LG:978182.4:2001MAR30	878	896	forward 1	TM	Transmembrane
91	LG:978182.4:2001MAR30	897	910	forward 1	TM	Non-Cytosolic
91	LG:978182.4:2001MAR30	911	933	forward 1	TM	Transmembrane
91	LG:978182.4:2001MAR30	934	971	forward 1	TM	Cytosolic
91	LG:978182.4:2001MAR30	972	994	forward 1	TM	Transmembrane
91	LG:978182.4:2001MAR30	995	1008	forward 1	TM	Non-Cytosolic
91	LG:978182.4:2001MAR30	1009	1031	forward 1	TM	Transmembrane
91	LG:978182.4:2001MAR30	1032	1410	forward 1	TM	Cytosolic
91	LG:978182.4:2001MAR30	1411	1428	forward 1	TM	Transmembrane
91	LG:978182.4:2001MAR30	1429	1429	forward 1	TM	Non-Cytosolic
91	LG:978182.4:2001MAR30	1	819	forward 2	TM	Non-Cytosolic
91	LG:978182.4:2001MAR30	820	842	forward 2	TM	Transmembrane
91	LG:978182.4:2001MAR30	843	848	forward 2	TM	Cytosolic
91	LG:978182.4:2001MAR30	849	871	forward 2	TM	Transmembrane
91	LG:978182.4:2001MAR30	872	899	forward 2	TM	Non-Cytosolic
91	LG:978182.4:2001MAR30	900	922	forward 2	TM	Transmembrane
91	LG:978182.4:2001MAR30	923	966	forward 2	TM	Cytosolic
91	LG:978182.4:2001MAR30	967	989	forward 2	TM	Transmembrane
91	LG:978182.4:2001MAR30	990	998	forward 2	TM	Non-Cytosolic
91	LG:978182.4:2001MAR30	999	1018	forward 2	TM	Transmembrane
91	LG:978182.4:2001MAR30	1019	1202	forward 2	TM	Cytosolic
91	LG:978182.4:2001MAR30	1203	1225	forward 2	TM	Transmembrane
91	LG:978182.4:2001MAR30	1226	1429	forward 2	TM	Non-Cytosolic
91	LG:978182.4:2001MAR30	1	904	forward 3	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
91	LG:978182.4:2001MAR30	905	922	forward 3	TM	Transmembrane
91	LG:978182.4:2001MAR30	923	966	forward 3	TM	Cytosolic
91	LG:978182.4:2001MAR30	967	989	forward 3	TM	Transmembrane
91	LG:978182.4:2001MAR30	990	992	forward 3	TM	Non-Cytosolic
91	LG:978182.4:2001MAR30	993	1015	forward 3	TM	Transmembrane
91	LG:978182.4:2001MAR30	1016	1035	forward 3	TM	Cytosolic
91	LG:978182.4:2001MAR30	1036	1058	forward 3	TM	Transmembrane
91	LG:978182.4:2001MAR30	1059	1429	forward 3	TM	Non-Cytosolic
92	LG:986827.1:2001MAR30	1	363	forward 1	TM	Non-Cytosolic
92	LG:986827.1:2001MAR30	364	386	forward 1	TM	Transmembrane
92	LG:986827.1:2001MAR30	387	401	forward 1	TM	Cytosolic
93	LG:013792.1:2001MAR30	1	124	forward 1	TM	Cytosolic
93	LG:013792.1:2001MAR30	125	147	forward 1	TM	Transmembrane
93	LG:013792.1:2001MAR30	148	184	forward 1	TM	Non-Cytosolic
93	LG:013792.1:2001MAR30	185	207	forward 1	TM	Transmembrane
93	LG:013792.1:2001MAR30	208	265	forward 1	TM	Cytosolic
93	LG:013792.1:2001MAR30	266	288	forward 1	TM	Transmembrane
93	LG:013792.1:2001MAR30	289	539	forward 1	TM	Non-Cytosolic
94	LG:018258.1:2001MAR30	1	9	forward 2	TM	Non-Cytosolic
94	LG:018258.1:2001MAR30	10	28	forward 2	TM	Transmembrane
94	LG:018258.1:2001MAR30	29	218	forward 2	TM	Cytosolic
94	LG:018258.1:2001MAR30	219	241	forward 2	TM	Transmembrane
94	LG:018258.1:2001MAR30	242	244	forward 2	TM	Non-Cytosolic
95	LG:023126.3:2001MAR30	1	470	forward 1	TM	Non-Cytosolic
95	LG:023126.3:2001MAR30	471	493	forward 1	TM	Transmembrane
95	LG:023126.3:2001MAR30	494	530	forward 1	TM	Cytosolic
96	LG:023618.1:2001MAR30	1	12	forward 3	TM	Cytosolic
96	LG:023618.1:2001MAR30	13	35	forward 3	TM	Transmembrane
96	LG:023618.1:2001MAR30	36	1625	forward 3	TM	Non-Cytosolic
96	LG:023618.1:2001MAR30	1626	1648	forward 3	TM	Transmembrane
96	LG:023618.1:2001MAR30	1649	1654	forward 3	TM	Cytosolic
96	LG:023618.1:2001MAR30	1655	1677	forward 3	TM	Transmembrane
96	LG:023618.1:2001MAR30	1678	2153	forward 3	TM	Non-Cytosolic
97	LG:030999.1:2001MAR30	1	791	forward 3	TM	Non-Cytosolic
97	LG:030999.1:2001MAR30	792	814	forward 3	TM	Transmembrane
97	LG:030999.1:2001MAR30	815	882	forward 3	TM	Cytosolic
98	LG:103508.1:2001MAR30	1	324	forward 1	TM	Cytosolic
98	LG:103508.1:2001MAR30	325	347	forward 1	TM	Transmembrane
98	LG:103508.1:2001MAR30	348	351	forward 1	TM	Non-Cytosolic
98	LG:103508.1:2001MAR30	352	371	forward 1	TM	Transmembrane
98	LG:103508.1:2001MAR30	372	460	forward 1	TM	Cytosolic
99	LG:107976.15:2001MAR30	1	2507	forward 1	TM	Non-Cytosolic
99	LG:107976.15:2001MAR30	2508	2530	forward 1	TM	Transmembrane
99	LG:107976.15:2001MAR30	2531	2687	forward 1	TM	Cytosolic
99	LG:107976.15:2001MAR30	1	2506	forward 2	TM	Non-Cytosolic
99	LG:107976.15:2001MAR30	2507	2529	forward 2	TM	Transmembrane
99	LG:107976.15:2001MAR30	2530	2579	forward 2	TM	Cytosolic
99	LG:107976.15:2001MAR30	2580	2602	forward 2	TM	Transmembrane
99	LG:107976.15:2001MAR30	2603	2687	forward 2	TM	Non-Cytosolic
99	LG:107976.15:2001MAR30	1	2583	forward 3	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
99	LG:107976.15:2001MAR30	2584	2606	forward 3	TM	Transmembrane
99	LG:107976.15:2001MAR30	2607	2625	forward 3	TM	Cytosolic
99	LG:107976.15:2001MAR30	2626	2645	forward 3	TM	Transmembrane
99	LG:107976.15:2001MAR30	2646	2686	forward 3	TM	Non-Cytosolic
100	LG:1080096.1:2001MAR30	1	6	forward 2	TM	Cytosolic
100	LG:1080096.1:2001MAR30	7	29	forward 2	TM	Transmembrane
100	LG:1080096.1:2001MAR30	30	51	forward 2	TM	Non-Cytosolic
100	LG:1080096.1:2001MAR30	52	74	forward 2	TM	Transmembrane
100	LG:1080096.1:2001MAR30	75	172	forward 2	TM	Cytosolic
100	LG:1080096.1:2001MAR30	173	195	forward 2	TM	Transmembrane
100	LG:1080096.1:2001MAR30	196	676	forward 2	TM	Non-Cytosolic
100	LG:1080096.1:2001MAR30	677	699	forward 2	TM	Transmembrane
100	LG:1080096.1:2001MAR30	700	719	forward 2	TM	Cytosolic
100	LG:1080096.1:2001MAR30	720	737	forward 2	TM	Transmembrane
100	LG:1080096.1:2001MAR30	738	777	forward 2	TM	Non-Cytosolic
100	LG:1080096.1:2001MAR30	778	797	forward 2	TM	Transmembrane
100	LG:1080096.1:2001MAR30	798	928	forward 2	TM	Cytosolic
100	LG:1080096.1:2001MAR30	1	6	forward 3	TM	Cytosolic
100	LG:1080096.1:2001MAR30	7	29	forward 3	TM	Transmembrane
100	LG:1080096.1:2001MAR30	30	48	forward 3	TM	Non-Cytosolic
100	LG:1080096.1:2001MAR30	49	71	forward 3	TM	Transmembrane
100	LG:1080096.1:2001MAR30	72	776	forward 3	TM	Cytosolic
100	LG:1080096.1:2001MAR30	777	799	forward 3	TM	Transmembrane
100	LG:1080096.1:2001MAR30	800	818	forward 3	TM	Non-Cytosolic
100	LG:1080096.1:2001MAR30	819	841	forward 3	TM	Transmembrane
100	LG:1080096.1:2001MAR30	842	927	forward 3	TM	Cytosolic
101	LG:1080275.1:2001MAR30	1	252	forward 1	TM	Cytosolic
101	LG:1080275.1:2001MAR30	253	275	forward 1	TM	Transmembrane
101	LG:1080275.1:2001MAR30	276	380	forward 1	TM	Non-Cytosolic
102	LG:1090358.10:2001MAR30	1	3	forward 1	TM	Non-Cytosolic
102	LG:1090358.10:2001MAR30	4	26	forward 1	TM	Transmembrane
102	LG:1090358.10:2001MAR30	27	30	forward 1	TM	Cytosolic
102	LG:1090358.10:2001MAR30	31	53	forward 1	TM	Transmembrane
102	LG:1090358.10:2001MAR30	54	597	forward 1	TM	Non-Cytosolic
102	LG:1090358.10:2001MAR30	1	3	forward 2	TM	Non-Cytosolic
102	LG:1090358.10:2001MAR30	4	26	forward 2	TM	Transmembrane
102	LG:1090358.10:2001MAR30	27	32	forward 2	TM	Cytosolic
102	LG:1090358.10:2001MAR30	33	55	forward 2	TM	Transmembrane
102	LG:1090358.10:2001MAR30	56	597	forward 2	TM	Non-Cytosolic
103	LG:1095833.9:2001MAR30	1	1721	forward 1	TM	Non-Cytosolic
103	LG:1095833.9:2001MAR30	1722	1744	forward 1	TM	Transmembrane
103	LG:1095833.9:2001MAR30	1745	1763	forward 1	TM	Cytosolic
103	LG:1095833.9:2001MAR30	1764	1786	forward 1	TM	Transmembrane
103	LG:1095833.9:2001MAR30	1787	1923	forward 1	TM	Non-Cytosolic
103	LG:1095833.9:2001MAR30	1924	1943	forward 1	TM	Transmembrane
103	LG:1095833.9:2001MAR30	1944	2097	forward 1	TM	Cytosolic
103	LG:1095833.9:2001MAR30	2098	2120	forward 1	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2121	2165	forward 1	TM	Non-Cytosolic
103	LG:1095833.9:2001MAR30	2166	2188	forward 1	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2189	2207	forward 1	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
103	LG:1095833.9:2001MAR30	2208	2230	forward 1	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2231	2283	forward 1	TM	Non-Cytosolic
103	LG:1095833.9:2001MAR30	2284	2303	forward 1	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2304	2323	forward 1	TM	Cytosolic
103	LG:1095833.9:2001MAR30	2324	2343	forward 1	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2344	2352	forward 1	TM	Non-Cytosolic
103	LG:1095833.9:2001MAR30	2353	2375	forward 1	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2376	2439	forward 1	TM	Cytosolic
103	LG:1095833.9:2001MAR30	2440	2462	forward 1	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2463	2481	forward 1	TM	Non-Cytosolic
103	LG:1095833.9:2001MAR30	2482	2504	forward 1	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2505	2562	forward 1	TM	Cytosolic
103	LG:1095833.9:2001MAR30	2563	2580	forward 1	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2581	2589	forward 1	TM	Non-Cytosolic
103	LG:1095833.9:2001MAR30	2590	2612	forward 1	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2613	2659	forward 1	TM	Cytosolic
103	LG:1095833.9:2001MAR30	2660	2682	forward 1	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2683	2777	forward 1	TM	Non-Cytosolic
103	LG:1095833.9:2001MAR30	2778	2800	forward 1	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2801	2806	forward 1	TM	Cytosolic
103	LG:1095833.9:2001MAR30	2807	2829	forward 1	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2830	2848	forward 1	TM	Non-Cytosolic
103	LG:1095833.9:2001MAR30	2849	2867	forward 1	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2868	2887	forward 1	TM	Cytosolic
103	LG:1095833.9:2001MAR30	2888	2910	forward 1	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2911	2939	forward 1	TM	Non-Cytosolic
103	LG:1095833.9:2001MAR30	2940	2962	forward 1	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2963	2982	forward 1	TM	Cytosolic
103	LG:1095833.9:2001MAR30	2983	3005	forward 1	TM	Transmembrane
103	LG:1095833.9:2001MAR30	3006	3065	forward 1	TM	Non-Cytosolic
103	LG:1095833.9:2001MAR30	3066	3088	forward 1	TM	Transmembrane
103	LG:1095833.9:2001MAR30	3089	3161	forward 1	TM	Cytosolic
103	LG:1095833.9:2001MAR30	3162	3184	forward 1	TM	Transmembrane
103	LG:1095833.9:2001MAR30	3185	3185	forward 1	TM	Non-Cytosolic
103	LG:1095833.9:2001MAR30	1	1762	forward 2	TM	Non-Cytosolic
103	LG:1095833.9:2001MAR30	1763	1785	forward 2	TM	Transmembrane
103	LG:1095833.9:2001MAR30	1786	1796	forward 2	TM	Cytosolic
103	LG:1095833.9:2001MAR30	1797	1819	forward 2	TM	Transmembrane
103	LG:1095833.9:2001MAR30	1820	1920	forward 2	TM	Non-Cytosolic
103	LG:1095833.9:2001MAR30	1921	1943	forward 2	TM	Transmembrane
103	LG:1095833.9:2001MAR30	1944	2138	forward 2	TM	Cytosolic
103	LG:1095833.9:2001MAR30	2139	2161	forward 2	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2162	2170	forward 2	TM	Non-Cytosolic
103	LG:1095833.9:2001MAR30	2171	2189	forward 2	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2190	2201	forward 2	TM	Cytosolic
103	LG:1095833.9:2001MAR30	2202	2224	forward 2	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2225	2283	forward 2	TM	Non-Cytosolic
103	LG:1095833.9:2001MAR30	2284	2303	forward 2	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2304	2307	forward 2	TM	Cytosolic
103	LG:1095833.9:2001MAR30	2308	2330	forward 2	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
103	LG:1095833.9:2001MAR30	2331	2435	forward 2	TM	Non-Cytosolic
103	LG:1095833.9:2001MAR30	2436	2458	forward 2	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2459	2631	forward 2	TM	Cytosolic
103	LG:1095833.9:2001MAR30	2632	2654	forward 2	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2655	2673	forward 2	TM	Non-Cytosolic
103	LG:1095833.9:2001MAR30	2674	2696	forward 2	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2697	2715	forward 2	TM	Cytosolic
103	LG:1095833.9:2001MAR30	2716	2733	forward 2	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2734	2769	forward 2	TM	Non-Cytosolic
103	LG:1095833.9:2001MAR30	2770	2789	forward 2	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2790	2800	forward 2	TM	Cytosolic
103	LG:1095833.9:2001MAR30	2801	2823	forward 2	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2824	2835	forward 2	TM	Non-Cytosolic
103	LG:1095833.9:2001MAR30	2836	2858	forward 2	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2859	2898	forward 2	TM	Cytosolic
103	LG:1095833.9:2001MAR30	2899	2921	forward 2	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2922	2940	forward 2	TM	Non-Cytosolic
103	LG:1095833.9:2001MAR30	2941	2963	forward 2	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2964	3048	forward 2	TM	Cytosolic
103	LG:1095833.9:2001MAR30	3049	3071	forward 2	TM	Transmembrane
103	LG:1095833.9:2001MAR30	3072	3184	forward 2	TM	Non-Cytosolic
103	LG:1095833.9:2001MAR30	1	1712	forward 3	TM	Non-Cytosolic
103	LG:1095833.9:2001MAR30	1713	1735	forward 3	TM	Transmembrane
103	LG:1095833.9:2001MAR30	1736	1755	forward 3	TM	Cytosolic
103	LG:1095833.9:2001MAR30	1756	1778	forward 3	TM	Transmembrane
103	LG:1095833.9:2001MAR30	1779	1855	forward 3	TM	Non-Cytosolic
103	LG:1095833.9:2001MAR30	1856	1878	forward 3	TM	Transmembrane
103	LG:1095833.9:2001MAR30	1879	1889	forward 3	TM	Cytosolic
103	LG:1095833.9:2001MAR30	1890	1907	forward 3	TM	Transmembrane
103	LG:1095833.9:2001MAR30	1908	1921	forward 3	TM	Non-Cytosolic
103	LG:1095833.9:2001MAR30	1922	1941	forward 3	TM	Transmembrane
103	LG:1095833.9:2001MAR30	1942	2022	forward 3	TM	Cytosolic
103	LG:1095833.9:2001MAR30	2023	2045	forward 3	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2046	2107	forward 3	TM	Non-Cytosolic
103	LG:1095833.9:2001MAR30	2108	2127	forward 3	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2128	2138	forward 3	TM	Cytosolic
103	LG:1095833.9:2001MAR30	2139	2161	forward 3	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2162	2175	forward 3	TM	Non-Cytosolic
103	LG:1095833.9:2001MAR30	2176	2198	forward 3	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2199	2210	forward 3	TM	Cytosolic
103	LG:1095833.9:2001MAR30	2211	2230	forward 3	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2231	2285	forward 3	TM	Non-Cytosolic
103	LG:1095833.9:2001MAR30	2286	2308	forward 3	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2309	2328	forward 3	TM	Cytosolic
103	LG:1095833.9:2001MAR30	2329	2351	forward 3	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2352	2441	forward 3	TM	Non-Cytosolic
103	LG:1095833.9:2001MAR30	2442	2464	forward 3	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2465	2470	forward 3	TM	Cytosolic
103	LG:1095833.9:2001MAR30	2471	2489	forward 3	TM	Transmembrane
103	LG:1095833.9:2001MAR30	2490	2555	forward 3	TM	Non-Cytosolic

Table 5

2604-2862; 2622-3122; 2630-2892; 2630-3177; 2633-2861; 2660-3166; 2674-3099; 2684-3196; 2701-2948; 2704-3189; 2713-3104; 2718-3197; 2722-2960; 2722-2968; 2760-3210; 2770-3209; 2773-3015; 2779-3170; 2783-3210; 2796-3030; 2801-3206; 2812-3215; 2815-3199; 2816-3087; 2822-3212; 2823-3210; 2824-3203; 2826-3212; 2830-3206; 2853-3115; 2855-3209; 2864-3204; 2864-3201; 2864-3210; 2864-3209; 2866-3212; 2884-3078; 2878-3209; 2889-3209; 2905-3209; 2907-3199; 2907-3170; 2915-3210; 2915-3173; 2920-3204; 2930-3209; 2937-3206; 2957-3210; 2960-3215; 2965-3184; 2967-3204; 2969-3209; 2970-3196; 2990-3209; 2995-3209; 3013-3196; 3018-3212; 3032-3208; 3054-3189; 3061-3206; 3067-3214; 3092-3209; 3158-3450

130/LG:332027.6:2001MAR30 || 1-539; 379-847; 392-608; 394-1148; 398-967; 422-1064; 428-787; 642-1264; 690-888; 838-1296; 897-1080; 982-1632; 1066-1632; 1104-1457; 1164-1453; 1370-1459; 1373-1619; 1495-1736; 1545-2138; 1575-1899; 1578-1765; 1618-1775; 1891-2407; 2032-2268; 2075-2447; 2082-2446; 2119-2523; 2126-2446; 2314-2550; 2491-2755; 2491-2889; 2503-2715; 2586-2953; 2586-2808; 2661-2929; 2674-2860; 2804-3042; 2870-3120; 2880-3286; 2929-3408; 2929-3128; 2949-3197; 2951-3195; 2973-3425; 2973-3116; 3023-3338; 3028-3267; 3067-3328; 3070-3304; 3120-3347; 3194-3417; 3195-3417; 3218-3368; 3223-3372; 3226-3368; 3234-3368; 3251-3417; 3279-3370; 3302-3370; 3315-3368; 3325-3456; 3373-3456

131/LG:336998.1:2001MAR30 || 1-5526; 1-11708; 30-516; 30-512; 30-471; 30-353; 30-156; 30-477; 30-465; 31-260; 39-651; 96-530; 98-534; 106-527; 107-412; 120-462; 131-609; 157-384; 182-373; 224-489; 261-396; 296-610; 413-556; 455-606; 448-707; 448-664; 463-839; 609-1104; 632-948; 692-1273; 889-1349; 897-1365; 916-1474; 929-1367; 963-1509; 1022-1410; 1052-1475; 1127-1489; 1161-1426; 1202-1771; 1279-1668; 1284-1735; 1309-1852; 1355-1759; 1408-1680; 1408-1643; 1543-1999; 1571-2182; 1576-1747; 1609-1993; 1611-1997; 1627-1838; 1642-2110; 1653-1993; 1731-1997; 1733-1994; 1747-1997; 1751-1993; 1866-2290; 1882-2427; 1968-2265; 1971-2417; 1975-2417; 2045-2417; 2142-2402; 2208-2706; 2268-2809; 2431-2955; 2439-2688; 2504-2793; 2532-2671; 2570-3071; 2605-3199; 2605-2689; 2623-3058; 2682-3082; 2727-2979; 2750-3088; 2788-3398; 2950-3434; 2955-3437; 2954-3225; 2984-3437; 2992-3437; 3046-3265; 3044-3195; 3046-3437; 3059-3264; 3080-3437; 3091-3437; 3167-3438; 3173-3419; 3187-3457; 3233-3556; 3450-3867; 3745-6783; 3846-4092; 3964-4354; 4059-4418; 4077-4369; 4135-4350; 4144-4354; 4330-4762; 4861-5175; 5364-5865; 5589-6148; 5721-6290; 5815-6398; 6191-6796; 6255-6859; 6280-6825; 6504-7063; 6531-6850; 6543-6850; 6552-6850; 6556-6847; 6580-6851; 6595-6850; 6611-6848; 6630-6853; 6701-7376; 7013-7651; 7526-8129; 7627-8020; 7717-8020; 7833-8020; 7837-8492; 7887-8143; 7916-8184; 8289-8881; 8434-8984; 8501-9044; 8526-9080; 8586-8830; 8669-9231; 8782-9184; 8794-9184; 8814-9110; 9008-9559; 9024-9238; 9050-9401; 9047-9280; 9131-9484; 9137-9480; 9347-9484; 9471-9741; 9646-10042; 9850-10451; 9849-10320; 9850-10441; 9898-10176; 10126-10441; 10439-10927; 10439-10867; 10459-10739; 10461-10712; 10487-10727; 10586-10780; 10853-11006; 10938-11341; 10990-11491; 11113-11388; 11155-11381; 11181-11725; 11216-11860; 11260-11793; 11264-11707; 11266-11550; 11269-11731; 11689-11952; 11748-12262; 11897-12132; 11990-12583; 12017-12281; 12125-12684; 12125-12638; 12125-12377; 12128-12643; 12136-12718; 12214-12499; 12230-12446; 12245-12889; 12251-12394; 12251-12453; 12323-12548; 12326-12576; 12400-12915; 12398-12704; 12418-12850; 12493-12636; 12541-12731; 12611-13040; 12616-12912; 12617-12790; 12619-13154; 12635-12979; 12702-13152; 12718-12969; 12730-13049; 12865-13167; 12948-13164; 12955-13560; 12965-13253; 13023-13285; 13027-13222; 13030-13489; 13077-13357; 13104-13440; 13114-13399; 13115-13378; 13130-13545; 13134-13461; 13142-13458; 13152-13744; 13153-13455; 13169-13553; 13175-13633; 13198-13455; 13204-13492; 13213-13478; 13216-13511; 13235-13481; 13252-13728; 13252-13497; 13309-13571; 13316-13520; 13347-13562; 13370-13611; 13394-13452; 13400-13694; 13404-13982; 13443-13666; 13455-13947; 13461-14005; 13485-14055; 13485-13756; 13529-14137; 13540-14150; 13543-13767; 13546-13873; 13583-13829; 13589-13874; 13589-13740; 13592-14132; 13606-13687; 13609-13864; 13613-14123; 13622-

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
105	LG:1386609.2:2001MAR30	1327	1345	forward 2	TM	Non-Cytosolic
105	LG:1386609.2:2001MAR30	1346	1368	forward 2	TM	Transmembrane
105	LG:1386609.2:2001MAR30	1369	1380	forward 2	TM	Cytosolic
105	LG:1386609.2:2001MAR30	1381	1403	forward 2	TM	Transmembrane
105	LG:1386609.2:2001MAR30	1404	1417	forward 2	TM	Non-Cytosolic
105	LG:1386609.2:2001MAR30	1418	1440	forward 2	TM	Transmembrane
105	LG:1386609.2:2001MAR30	1441	1452	forward 2	TM	Cytosolic
105	LG:1386609.2:2001MAR30	1453	1475	forward 2	TM	Transmembrane
105	LG:1386609.2:2001MAR30	1476	1750	forward 2	TM	Non-Cytosolic
105	LG:1386609.2:2001MAR30	1751	1773	forward 2	TM	Transmembrane
105	LG:1386609.2:2001MAR30	1774	1824	forward 2	TM	Cytosolic
105	LG:1386609.2:2001MAR30	1825	1847	forward 2	TM	Transmembrane
105	LG:1386609.2:2001MAR30	1848	2529	forward 2	TM	Non-Cytosolic
105	LG:1386609.2:2001MAR30	2530	2552	forward 2	TM	Transmembrane
105	LG:1386609.2:2001MAR30	2553	2756	forward 2	TM	Cytosolic
105	LG:1386609.2:2001MAR30	2757	2779	forward 2	TM	Transmembrane
105	LG:1386609.2:2001MAR30	2780	3077	forward 2	TM	Non-Cytosolic
105	LG:1386609.2:2001MAR30	1	1600	forward 3	TM	Non-Cytosolic
105	LG:1386609.2:2001MAR30	1601	1623	forward 3	TM	Transmembrane
105	LG:1386609.2:2001MAR30	1624	1754	forward 3	TM	Cytosolic
105	LG:1386609.2:2001MAR30	1755	1777	forward 3	TM	Transmembrane
105	LG:1386609.2:2001MAR30	1778	2315	forward 3	TM	Non-Cytosolic
105	LG:1386609.2:2001MAR30	2316	2338	forward 3	TM	Transmembrane
105	LG:1386609.2:2001MAR30	2339	2374	forward 3	TM	Cytosolic
105	LG:1386609.2:2001MAR30	2375	2397	forward 3	TM	Transmembrane
105	LG:1386609.2:2001MAR30	2398	2722	forward 3	TM	Non-Cytosolic
105	LG:1386609.2:2001MAR30	2723	2742	forward 3	TM	Transmembrane
105	LG:1386609.2:2001MAR30	2743	2754	forward 3	TM	Cytosolic
105	LG:1386609.2:2001MAR30	2755	2774	forward 3	TM	Transmembrane
105	LG:1386609.2:2001MAR30	2775	3076	forward 3	TM	Non-Cytosolic
106	LG:1398465.1:2001MAR30	1	111	forward 1	TM	Cytosolic
106	LG:1398465.1:2001MAR30	112	134	forward 1	TM	Transmembrane
106	LG:1398465.1:2001MAR30	135	169	forward 1	TM	Non-Cytosolic
106	LG:1398465.1:2001MAR30	170	192	forward 1	TM	Transmembrane
106	LG:1398465.1:2001MAR30	193	204	forward 1	TM	Cytosolic
106	LG:1398465.1:2001MAR30	205	227	forward 1	TM	Transmembrane
106	LG:1398465.1:2001MAR30	228	246	forward 1	TM	Non-Cytosolic
106	LG:1398465.1:2001MAR30	247	269	forward 1	TM	Transmembrane
106	LG:1398465.1:2001MAR30	270	275	forward 1	TM	Cytosolic
106	LG:1398465.1:2001MAR30	276	298	forward 1	TM	Transmembrane
106	LG:1398465.1:2001MAR30	299	384	forward 1	TM	Non-Cytosolic
106	LG:1398465.1:2001MAR30	385	407	forward 1	TM	Transmembrane
106	LG:1398465.1:2001MAR30	408	449	forward 1	TM	Cytosolic
106	LG:1398465.1:2001MAR30	450	472	forward 1	TM	Transmembrane
106	LG:1398465.1:2001MAR30	473	521	forward 1	TM	Non-Cytosolic
106	LG:1398465.1:2001MAR30	522	544	forward 1	TM	Transmembrane
106	LG:1398465.1:2001MAR30	545	630	forward 1	TM	Cytosolic
106	LG:1398465.1:2001MAR30	631	653	forward 1	TM	Transmembrane
106	LG:1398465.1:2001MAR30	654	657	forward 1	TM	Non-Cytosolic
106	LG:1398465.1:2001MAR30	658	675	forward 1	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
106	LG:1398465.1:2001MAR30	676	695	forward 1	TM	Cytosolic
106	LG:1398465.1:2001MAR30	696	718	forward 1	TM	Transmembrane
106	LG:1398465.1:2001MAR30	719	748	forward 1	TM	Non-Cytosolic
106	LG:1398465.1:2001MAR30	749	771	forward 1	TM	Transmembrane
106	LG:1398465.1:2001MAR30	772	791	forward 1	TM	Cytosolic
106	LG:1398465.1:2001MAR30	792	814	forward 1	TM	Transmembrane
106	LG:1398465.1:2001MAR30	815	823	forward 1	TM	Non-Cytosolic
106	LG:1398465.1:2001MAR30	824	846	forward 1	TM	Transmembrane
106	LG:1398465.1:2001MAR30	847	1087	forward 1	TM	Cytosolic
106	LG:1398465.1:2001MAR30	1088	1110	forward 1	TM	Transmembrane
106	LG:1398465.1:2001MAR30	1111	1113	forward 1	TM	Non-Cytosolic
106	LG:1398465.1:2001MAR30	1114	1136	forward 1	TM	Transmembrane
106	LG:1398465.1:2001MAR30	1137	1152	forward 1	TM	Cytosolic
106	LG:1398465.1:2001MAR30	1	205	forward 2	TM	Non-Cytosolic
106	LG:1398465.1:2001MAR30	206	228	forward 2	TM	Transmembrane
106	LG:1398465.1:2001MAR30	229	374	forward 2	TM	Cytosolic
106	LG:1398465.1:2001MAR30	375	397	forward 2	TM	Transmembrane
106	LG:1398465.1:2001MAR30	398	443	forward 2	TM	Non-Cytosolic
106	LG:1398465.1:2001MAR30	444	466	forward 2	TM	Transmembrane
106	LG:1398465.1:2001MAR30	467	633	forward 2	TM	Cytosolic
106	LG:1398465.1:2001MAR30	634	656	forward 2	TM	Transmembrane
106	LG:1398465.1:2001MAR30	657	696	forward 2	TM	Non-Cytosolic
106	LG:1398465.1:2001MAR30	697	719	forward 2	TM	Transmembrane
106	LG:1398465.1:2001MAR30	720	725	forward 2	TM	Cytosolic
106	LG:1398465.1:2001MAR30	726	743	forward 2	TM	Transmembrane
106	LG:1398465.1:2001MAR30	744	746	forward 2	TM	Non-Cytosolic
106	LG:1398465.1:2001MAR30	747	769	forward 2	TM	Transmembrane
106	LG:1398465.1:2001MAR30	770	808	forward 2	TM	Cytosolic
106	LG:1398465.1:2001MAR30	809	831	forward 2	TM	Transmembrane
106	LG:1398465.1:2001MAR30	832	859	forward 2	TM	Non-Cytosolic
106	LG:1398465.1:2001MAR30	860	882	forward 2	TM	Transmembrane
106	LG:1398465.1:2001MAR30	883	954	forward 2	TM	Cytosolic
106	LG:1398465.1:2001MAR30	955	977	forward 2	TM	Transmembrane
106	LG:1398465.1:2001MAR30	978	1060	forward 2	TM	Non-Cytosolic
106	LG:1398465.1:2001MAR30	1061	1082	forward 2	TM	Transmembrane
106	LG:1398465.1:2001MAR30	1083	1152	forward 2	TM	Cytosolic
106	LG:1398465.1:2001MAR30	1	520	forward 3	TM	Non-Cytosolic
106	LG:1398465.1:2001MAR30	521	543	forward 3	TM	Transmembrane
106	LG:1398465.1:2001MAR30	544	583	forward 3	TM	Cytosolic
106	LG:1398465.1:2001MAR30	584	606	forward 3	TM	Transmembrane
106	LG:1398465.1:2001MAR30	607	627	forward 3	TM	Non-Cytosolic
106	LG:1398465.1:2001MAR30	628	650	forward 3	TM	Transmembrane
106	LG:1398465.1:2001MAR30	651	658	forward 3	TM	Cytosolic
106	LG:1398465.1:2001MAR30	659	681	forward 3	TM	Transmembrane
106	LG:1398465.1:2001MAR30	682	700	forward 3	TM	Non-Cytosolic
106	LG:1398465.1:2001MAR30	701	718	forward 3	TM	Transmembrane
106	LG:1398465.1:2001MAR30	719	724	forward 3	TM	Cytosolic
106	LG:1398465.1:2001MAR30	725	747	forward 3	TM	Transmembrane
106	LG:1398465.1:2001MAR30	748	789	forward 3	TM	Non-Cytosolic
106	LG:1398465.1:2001MAR30	790	812	forward 3	TM	Transmembrane



TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
106	LG:1398465.1:2001MAR30	813	831	forward 3	TM	Cytosolic
106	LG:1398465.1:2001MAR30	832	851	forward 3	TM	Transmembrane
106	LG:1398465.1:2001MAR30	852	865	forward 3	TM	Non-Cytosolic
106	LG:1398465.1:2001MAR30	866	888	forward 3	TM	Transmembrane
106	LG:1398465.1:2001MAR30	889	1103	forward 3	TM	Cytosolic
106	LG:1398465.1:2001MAR30	1104	1126	forward 3	TM	Transmembrane
106	LG:1398465.1:2001MAR30	1127	1152	forward 3	TM	Non-Cytosolic
107	LG:1453417.10:2001MAR30	1	2349	forward 2	TM	Non-Cytosolic
107	LG:1453417.10:2001MAR30	2350	2372	forward 2	TM	Transmembrane
107	LG:1453417.10:2001MAR30	2373	2384	forward 2	TM	Cytosolic
107	LG:1453417.10:2001MAR30	2385	2404	forward 2	TM	Transmembrane
107	LG:1453417.10:2001MAR30	2405	2407	forward 2	TM	Non-Cytosolic
107	LG:1453417.10:2001MAR30	2408	2430	forward 2	TM	Transmembrane
107	LG:1453417.10:2001MAR30	2431	2450	forward 2	TM	Cytosolic
107	LG:1453417.10:2001MAR30	2451	2470	forward 2	TM	Transmembrane
107	LG:1453417.10:2001MAR30	2471	2489	forward 2	TM	Non-Cytosolic
107	LG:1453417.10:2001MAR30	2490	2512	forward 2	TM	Transmembrane
107	LG:1453417.10:2001MAR30	2513	2531	forward 2	TM	Cytosolic
107	LG:1453417.10:2001MAR30	2532	2554	forward 2	TM	Transmembrane
107	LG:1453417.10:2001MAR30	2555	3920	forward 2	TM	Non-Cytosolic
108	LG:147869.3:2001MAR30	1	88	forward 1	TM	Non-Cytosolic
108	LG:147869.3:2001MAR30	89	106	forward 1	TM	Transmembrane
108	LG:147869.3:2001MAR30	107	114	forward 1	TM	Cytosolic
108	LG:147869.3:2001MAR30	115	137	forward 1	TM	Transmembrane
108	LG:147869.3:2001MAR30	138	146	forward 1	TM	Non-Cytosolic
108	LG:147869.3:2001MAR30	147	169	forward 1	TM	Transmembrane
108	LG:147869.3:2001MAR30	170	189	forward 1	TM	Cytosolic
108	LG:147869.3:2001MAR30	190	212	forward 1	TM	Transmembrane
108	LG:147869.3:2001MAR30	213	226	forward 1	TM	Non-Cytosolic
108	LG:147869.3:2001MAR30	227	249	forward 1	TM	Transmembrane
108	LG:147869.3:2001MAR30	250	315	forward 1	TM	Cytosolic
108	LG:147869.3:2001MAR30	316	338	forward 1	TM	Transmembrane
108	LG:147869.3:2001MAR30	339	513	forward 1	TM	Non-Cytosolic
108	LG:147869.3:2001MAR30	514	536	forward 1	TM	Transmembrane
108	LG:147869.3:2001MAR30	537	540	forward 1	TM	Cytosolic
108	LG:147869.3:2001MAR30	541	563	forward 1	TM	Transmembrane
108	LG:147869.3:2001MAR30	564	572	forward 1	TM	Non-Cytosolic
108	LG:147869.3:2001MAR30	573	595	forward 1	TM	Transmembrane
108	LG:147869.3:2001MAR30	596	607	forward 1	TM	Cytosolic
108	LG:147869.3:2001MAR30	608	630	forward 1	TM	Transmembrane
108	LG:147869.3:2001MAR30	631	644	forward 1	TM	Non-Cytosolic
108	LG:147869.3:2001MAR30	645	667	forward 1	TM	Transmembrane
108	LG:147869.3:2001MAR30	668	713	forward 1	TM	Cytosolic
108	LG:147869.3:2001MAR30	1	564	forward 2	TM	Non-Cytosolic
108	LG:147869.3:2001MAR30	565	587	forward 2	TM	Transmembrane
108	LG:147869.3:2001MAR30	588	613	forward 2	TM	Cytosolic
108	LG:147869.3:2001MAR30	614	636	forward 2	TM	Transmembrane
108	LG:147869.3:2001MAR30	637	645	forward 2	TM	Non-Cytosolic
108	LG:147869.3:2001MAR30	646	665	forward 2	TM	Transmembrane
108	LG:147869.3:2001MAR30	666	685	forward 2	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
108	LG:147869.3:2001MAR30	686	708	forward 2	TM	Transmembrane
108	LG:147869.3:2001MAR30	709	713	forward 2	TM	Non-Cytosolic
109	LG:148485.5:2001MAR30	1	18	forward 1	TM	Cytosolic
109	LG:148485.5:2001MAR30	19	36	forward 1	TM	Transmembrane
109	LG:148485.5:2001MAR30	37	50	forward 1	TM	Non-Cytosolic
109	LG:148485.5:2001MAR30	51	73	forward 1	TM	Transmembrane
109	LG:148485.5:2001MAR30	74	189	forward 1	TM	Cytosolic
109	LG:148485.5:2001MAR30	190	212	forward 1	TM	Transmembrane
109	LG:148485.5:2001MAR30	213	288	forward 1	TM	Non-Cytosolic
109	LG:148485.5:2001MAR30	289	311	forward 1	TM	Transmembrane
109	LG:148485.5:2001MAR30	312	315	forward 1	TM	Cytosolic
110	LG:1501818.12:2001MAR30	1	177	forward 1	TM	Cytosolic
110	LG:1501818.12:2001MAR30	178	200	forward 1	TM	Transmembrane
110	LG:1501818.12:2001MAR30	201	571	forward 1	TM	Non-Cytosolic
110	LG:1501818.12:2001MAR30	1	446	forward 2	TM	Non-Cytosolic
110	LG:1501818.12:2001MAR30	447	469	forward 2	TM	Transmembrane
110	LG:1501818.12:2001MAR30	470	481	forward 2	TM	Cytosolic
110	LG:1501818.12:2001MAR30	482	501	forward 2	TM	Transmembrane
110	LG:1501818.12:2001MAR30	502	510	forward 2	TM	Non-Cytosolic
110	LG:1501818.12:2001MAR30	511	533	forward 2	TM	Transmembrane
110	LG:1501818.12:2001MAR30	534	570	forward 2	TM	Cytosolic
111	LG:1508275.1:2001MAR30	1	106	forward 1	TM	Cytosolic
112	LG:1509771.1:2001MAR30	1	134	forward 2	TM	Cytosolic
112	LG:1509771.1:2001MAR30	135	157	forward 2	TM	Transmembrane
112	LG:1509771.1:2001MAR30	158	159	forward 2	TM	Non-Cytosolic
113	LG:1512998.13:2001MAR30	1	597	forward 1	TM	Non-Cytosolic
113	LG:1512998.13:2001MAR30	598	620	forward 1	TM	Transmembrane
113	LG:1512998.13:2001MAR30	621	777	forward 1	TM	Cytosolic
113	LG:1512998.13:2001MAR30	778	800	forward 1	TM	Transmembrane
113	LG:1512998.13:2001MAR30	801	814	forward 1	TM	Non-Cytosolic
113	LG:1512998.13:2001MAR30	815	837	forward 1	TM	Transmembrane
113	LG:1512998.13:2001MAR30	838	935	forward 1	TM	Cytosolic
113	LG:1512998.13:2001MAR30	936	953	forward 1	TM	Transmembrane
113	LG:1512998.13:2001MAR30	954	1009	forward 1	TM	Non-Cytosolic
113	LG:1512998.13:2001MAR30	1010	1029	forward 1	TM	Transmembrane
113	LG:1512998.13:2001MAR30	1030	1049	forward 1	TM	Cytosolic
113	LG:1512998.13:2001MAR30	1050	1069	forward 1	TM	Transmembrane
113	LG:1512998.13:2001MAR30	1070	1083	forward 1	TM	Non-Cytosolic
113	LG:1512998.13:2001MAR30	1084	1106	forward 1	TM	Transmembrane
113	LG:1512998.13:2001MAR30	1107	1228	forward 1	TM	Cytosolic
113	LG:1512998.13:2001MAR30	1	470	forward 2	TM	Non-Cytosolic
113	LG:1512998.13:2001MAR30	471	493	forward 2	TM	Transmembrane
113	LG:1512998.13:2001MAR30	494	523	forward 2	TM	Cytosolic
113	LG:1512998.13:2001MAR30	524	546	forward 2	TM	Transmembrane
113	LG:1512998.13:2001MAR30	547	596	forward 2	TM	Non-Cytosolic
113	LG:1512998.13:2001MAR30	597	619	forward 2	TM	Transmembrane
113	LG:1512998.13:2001MAR30	620	804	forward 2	TM	Cytosolic
113	LG:1512998.13:2001MAR30	805	827	forward 2	TM	Transmembrane
113	LG:1512998.13:2001MAR30	828	934	forward 2	TM	Non-Cytosolic
113	LG:1512998.13:2001MAR30	935	954	forward 2	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
113	LG:1512998.13:2001MAR30	955	1016	forward 2	TM	Cytosolic
113	LG:1512998.13:2001MAR30	1017	1039	forward 2	TM	Transmembrane
113	LG:1512998.13:2001MAR30	1040	1228	forward 2	TM	Non-Cytosolic
113	LG:1512998.13:2001MAR30	1	865	forward 3	TM	Non-Cytosolic
113	LG:1512998.13:2001MAR30	866	888	forward 3	TM	Transmembrane
113	LG:1512998.13:2001MAR30	889	964	forward 3	TM	Cytosolic
113	LG:1512998.13:2001MAR30	965	987	forward 3	TM	Transmembrane
113	LG:1512998.13:2001MAR30	988	1001	forward 3	TM	Non-Cytosolic
113	LG:1512998.13:2001MAR30	1002	1024	forward 3	TM	Transmembrane
113	LG:1512998.13:2001MAR30	1025	1044	forward 3	TM	Cytosolic
113	LG:1512998.13:2001MAR30	1045	1067	forward 3	TM	Transmembrane
113	LG:1512998.13:2001MAR30	1068	1227	forward 3	TM	Non-Cytosolic
114	LG:198251.7:2001MAR30	1	607	forward 1	TM	Non-Cytosolic
114	LG:198251.7:2001MAR30	608	630	forward 1	TM	Transmembrane
114	LG:198251.7:2001MAR30	631	689	forward 1	TM	Cytosolic
114	LG:198251.7:2001MAR30	690	709	forward 1	TM	Transmembrane
114	LG:198251.7:2001MAR30	710	768	forward 1	TM	Non-Cytosolic
114	LG:198251.7:2001MAR30	769	791	forward 1	TM	Transmembrane
114	LG:198251.7:2001MAR30	792	896	forward 1	TM	Cytosolic
114	LG:198251.7:2001MAR30	897	919	forward 1	TM	Transmembrane
114	LG:198251.7:2001MAR30	920	1107	forward 1	TM	Non-Cytosolic
114	LG:198251.7:2001MAR30	1108	1130	forward 1	TM	Transmembrane
114	LG:198251.7:2001MAR30	1131	1186	forward 1	TM	Cytosolic
114	LG:198251.7:2001MAR30	1	595	forward 2	TM	Non-Cytosolic
114	LG:198251.7:2001MAR30	596	618	forward 2	TM	Transmembrane
114	LG:198251.7:2001MAR30	619	637	forward 2	TM	Cytosolic
114	LG:198251.7:2001MAR30	638	655	forward 2	TM	Transmembrane
114	LG:198251.7:2001MAR30	656	685	forward 2	TM	Non-Cytosolic
114	LG:198251.7:2001MAR30	686	708	forward 2	TM	Transmembrane
114	LG:198251.7:2001MAR30	709	1096	forward 2	TM	Cytosolic
114	LG:198251.7:2001MAR30	1097	1119	forward 2	TM	Transmembrane
114	LG:198251.7:2001MAR30	1120	1185	forward 2	TM	Non-Cytosolic
114	LG:198251.7:2001MAR30	1	877	forward 3	TM	Non-Cytosolic
114	LG:198251.7:2001MAR30	878	900	forward 3	TM	Transmembrane
114	LG:198251.7:2001MAR30	901	919	forward 3	TM	Cytosolic
114	LG:198251.7:2001MAR30	920	937	forward 3	TM	Transmembrane
114	LG:198251.7:2001MAR30	938	1185	forward 3	TM	Non-Cytosolic
115	LG:198296.1:2001MAR30	1	896	forward 1	TM	Non-Cytosolic
115	LG:198296.1:2001MAR30	897	914	forward 1	TM	Transmembrane
115	LG:198296.1:2001MAR30	915	920	forward 1	TM	Cytosolic
115	LG:198296.1:2001MAR30	921	943	forward 1	TM	Transmembrane
115	LG:198296.1:2001MAR30	944	1036	forward 1	TM	Non-Cytosolic
115	LG:198296.1:2001MAR30	1037	1059	forward 1	TM	Transmembrane
115	LG:198296.1:2001MAR30	1060	1127	forward 1	TM	Cytosolic
115	LG:198296.1:2001MAR30	1128	1150	forward 1	TM	Transmembrane
115	LG:198296.1:2001MAR30	1151	1188	forward 1	TM	Non-Cytosolic
115	LG:198296.1:2001MAR30	1	20	forward 2	TM	Cytosolic
115	LG:198296.1:2001MAR30	21	43	forward 2	TM	Transmembrane
115	LG:198296.1:2001MAR30	44	530	forward 2	TM	Non-Cytosolic
115	LG:198296.1:2001MAR30	531	553	forward 2	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
115	LG:198296.1:2001MAR30	554	573	forward 2	TM	Cytosolic
115	LG:198296.1:2001MAR30	574	596	forward 2	TM	Transmembrane
115	LG:198296.1:2001MAR30	597	605	forward 2	TM	Non-Cytosolic
115	LG:198296.1:2001MAR30	606	628	forward 2	TM	Transmembrane
115	LG:198296.1:2001MAR30	629	766	forward 2	TM	Cytosolic
115	LG:198296.1:2001MAR30	767	789	forward 2	TM	Transmembrane
115	LG:198296.1:2001MAR30	790	813	forward 2	TM	Non-Cytosolic
115	LG:198296.1:2001MAR30	814	836	forward 2	TM	Transmembrane
115	LG:198296.1:2001MAR30	837	1054	forward 2	TM	Cytosolic
115	LG:198296.1:2001MAR30	1055	1077	forward 2	TM	Transmembrane
115	LG:198296.1:2001MAR30	1078	1091	forward 2	TM	Non-Cytosolic
115	LG:198296.1:2001MAR30	1092	1114	forward 2	TM	Transmembrane
115	LG:198296.1:2001MAR30	1115	1126	forward 2	TM	Cytosolic
115	LG:198296.1:2001MAR30	1127	1149	forward 2	TM	Transmembrane
115	LG:198296.1:2001MAR30	1150	1188	forward 2	TM	Non-Cytosolic
115	LG:198296.1:2001MAR30	1	458	forward 3	TM	Non-Cytosolic
115	LG:198296.1:2001MAR30	459	481	forward 3	TM	Transmembrane
115	LG:198296.1:2001MAR30	482	524	forward 3	TM	Cytosolic
115	LG:198296.1:2001MAR30	525	547	forward 3	TM	Transmembrane
115	LG:198296.1:2001MAR30	548	921	forward 3	TM	Non-Cytosolic
115	LG:198296.1:2001MAR30	922	944	forward 3	TM	Transmembrane
115	LG:198296.1:2001MAR30	945	1137	forward 3	TM	Cytosolic
115	LG:198296.1:2001MAR30	1138	1160	forward 3	TM	Transmembrane
115	LG:198296.1:2001MAR30	1161	1187	forward 3	TM	Non-Cytosolic
116	LG:198876.13:2001MAR30	1	535	forward 1	TM	Cytosolic
116	LG:198876.13:2001MAR30	536	558	forward 1	TM	Transmembrane
116	LG:198876.13:2001MAR30	559	1162	forward 1	TM	Non-Cytosolic
116	LG:198876.13:2001MAR30	1163	1185	forward 1	TM	Transmembrane
116	LG:198876.13:2001MAR30	1186	1191	forward 1	TM	Cytosolic
116	LG:198876.13:2001MAR30	1192	1214	forward 1	TM	Transmembrane
116	LG:198876.13:2001MAR30	1215	1405	forward 1	TM	Non-Cytosolic
116	LG:198876.13:2001MAR30	1	539	forward 2	TM	Non-Cytosolic
116	LG:198876.13:2001MAR30	540	562	forward 2	TM	Transmembrane
116	LG:198876.13:2001MAR30	563	732	forward 2	TM	Cytosolic
116	LG:198876.13:2001MAR30	733	755	forward 2	TM	Transmembrane
116	LG:198876.13:2001MAR30	756	778	forward 2	TM	Non-Cytosolic
116	LG:198876.13:2001MAR30	779	801	forward 2	TM	Transmembrane
116	LG:198876.13:2001MAR30	802	1160	forward 2	TM	Cytosolic
116	LG:198876.13:2001MAR30	1161	1183	forward 2	TM	Transmembrane
116	LG:198876.13:2001MAR30	1184	1202	forward 2	TM	Non-Cytosolic
116	LG:198876.13:2001MAR30	1203	1222	forward 2	TM	Transmembrane
116	LG:198876.13:2001MAR30	1223	1380	forward 2	TM	Cytosolic
116	LG:198876.13:2001MAR30	1381	1398	forward 2	TM	Transmembrane
116	LG:198876.13:2001MAR30	1399	1404	forward 2	TM	Non-Cytosolic
116	LG:198876.13:2001MAR30	1	12	forward 3	TM	Cytosolic
116	LG:198876.13:2001MAR30	13	35	forward 3	TM	Transmembrane
116	LG:198876.13:2001MAR30	36	68	forward 3	TM	Non-Cytosolic
116	LG:198876.13:2001MAR30	69	91	forward 3	TM	Transmembrane
116	LG:198876.13:2001MAR30	92	537	forward 3	TM	Cytosolic
116	LG:198876.13:2001MAR30	538	560	forward 3	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
116	LG:198876.13:2001MAR30	561	726	forward 3	TM	Non-Cytosolic
116	LG:198876.13:2001MAR30	727	749	forward 3	TM	Transmembrane
116	LG:198876.13:2001MAR30	750	1190	forward 3	TM	Cytosolic
116	LG:198876.13:2001MAR30	1191	1210	forward 3	TM	Transmembrane
116	LG:198876.13:2001MAR30	1211	1224	forward 3	TM	Non-Cytosolic
116	LG:198876.13:2001MAR30	1225	1247	forward 3	TM	Transmembrane
116	LG:198876.13:2001MAR30	1248	1404	forward 3	TM	Cytosolic
117	LG:200704.1:2001MAR30	1	425	forward 1	TM	Non-Cytosolic
117	LG:200704.1:2001MAR30	426	448	forward 1	TM	Transmembrane
117	LG:200704.1:2001MAR30	449	559	forward 1	TM	Cytosolic
117	LG:200704.1:2001MAR30	560	582	forward 1	TM	Transmembrane
117	LG:200704.1:2001MAR30	583	626	forward 1	TM	Non-Cytosolic
117	LG:200704.1:2001MAR30	627	646	forward 1	TM	Transmembrane
117	LG:200704.1:2001MAR30	647	733	forward 1	TM	Cytosolic
118	LG:206593.3:2001MAR30	1	464	forward 2	TM	Non-Cytosolic
118	LG:206593.3:2001MAR30	465	484	forward 2	TM	Transmembrane
118	LG:206593.3:2001MAR30	485	516	forward 2	TM	Cytosolic
119	LG:223970.11:2001MAR30	1	90	forward 1	TM	Cytosolic
119	LG:223970.11:2001MAR30	91	113	forward 1	TM	Transmembrane
119	LG:223970.11:2001MAR30	114	1376	forward 1	TM	Non-Cytosolic
119	LG:223970.11:2001MAR30	1377	1399	forward 1	TM	Transmembrane
119	LG:223970.11:2001MAR30	1400	1461	forward 1	TM	Cytosolic
119	LG:223970.11:2001MAR30	1462	1484	forward 1	TM	Transmembrane
119	LG:223970.11:2001MAR30	1485	1509	forward 1	TM	Non-Cytosolic
119	LG:223970.11:2001MAR30	1510	1532	forward 1	TM	Transmembrane
119	LG:223970.11:2001MAR30	1533	1687	forward 1	TM	Cytosolic
119	LG:223970.11:2001MAR30	1688	1710	forward 1	TM	Transmembrane
119	LG:223970.11:2001MAR30	1711	1724	forward 1	TM	Non-Cytosolic
119	LG:223970.11:2001MAR30	1725	1747	forward 1	TM	Transmembrane
119	LG:223970.11:2001MAR30	1748	2013	forward 1	TM	Cytosolic
119	LG:223970.11:2001MAR30	2014	2036	forward 1	TM	Transmembrane
119	LG:223970.11:2001MAR30	2037	2341	forward 1	TM	Non-Cytosolic
119	LG:223970.11:2001MAR30	1	868	forward 2	TM	Non-Cytosolic
119	LG:223970.11:2001MAR30	869	891	forward 2	TM	Transmembrane
119	LG:223970.11:2001MAR30	892	903	forward 2	TM	Cytosolic
119	LG:223970.11:2001MAR30	904	923	forward 2	TM	Transmembrane
119	LG:223970.11:2001MAR30	924	927	forward 2	TM	Non-Cytosolic
119	LG:223970.11:2001MAR30	928	950	forward 2	TM	Transmembrane
119	LG:223970.11:2001MAR30	951	1265	forward 2	TM	Cytosolic
119	LG:223970.11:2001MAR30	1266	1288	forward 2	TM	Transmembrane
119	LG:223970.11:2001MAR30	1289	1302	forward 2	TM	Non-Cytosolic
119	LG:223970.11:2001MAR30	1303	1325	forward 2	TM	Transmembrane
119	LG:223970.11:2001MAR30	1326	1401	forward 2	TM	Cytosolic
119	LG:223970.11:2001MAR30	1402	1424	forward 2	TM	Transmembrane
119	LG:223970.11:2001MAR30	1425	1443	forward 2	TM	Non-Cytosolic
119	LG:223970.11:2001MAR30	1444	1466	forward 2	TM	Transmembrane
119	LG:223970.11:2001MAR30	1467	1498	forward 2	TM	Cytosolic
119	LG:223970.11:2001MAR30	1499	1516	forward 2	TM	Transmembrane
119	LG:223970.11:2001MAR30	1517	1528	forward 2	TM	Non-Cytosolic
119	LG:223970.11:2001MAR30	1529	1551	forward 2	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
119	LG:223970.11:2001MAR30	1552	1677	forward 2	TM	Cytosolic
119	LG:223970.11:2001MAR30	1678	1700	forward 2	TM	Transmembrane
119	LG:223970.11:2001MAR30	1701	2341	forward 2	TM	Non-Cytosolic
119	LG:223970.11:2001MAR30	1	622	forward 3	TM	Non-Cytosolic
119	LG:223970.11:2001MAR30	623	645	forward 3	TM	Transmembrane
119	LG:223970.11:2001MAR30	646	705	forward 3	TM	Cytosolic
119	LG:223970.11:2001MAR30	706	728	forward 3	TM	Transmembrane
119	LG:223970.11:2001MAR30	729	870	forward 3	TM	Non-Cytosolic
119	LG:223970.11:2001MAR30	871	893	forward 3	TM	Transmembrane
119	LG:223970.11:2001MAR30	894	899	forward 3	TM	Cytosolic
119	LG:223970.11:2001MAR30	900	922	forward 3	TM	Transmembrane
119	LG:223970.11:2001MAR30	923	927	forward 3	TM	Non-Cytosolic
119	LG:223970.11:2001MAR30	928	950	forward 3	TM	Transmembrane
119	LG:223970.11:2001MAR30	951	962	forward 3	TM	Cytosolic
119	LG:223970.11:2001MAR30	963	985	forward 3	TM	Transmembrane
119	LG:223970.11:2001MAR30	986	1024	forward 3	TM	Non-Cytosolic
119	LG:223970.11:2001MAR30	1025	1047	forward 3	TM	Transmembrane
119	LG:223970.11:2001MAR30	1048	1250	forward 3	TM	Cytosolic
119	LG:223970.11:2001MAR30	1251	1273	forward 3	TM	Transmembrane
119	LG:223970.11:2001MAR30	1274	1303	forward 3	TM	Non-Cytosolic
119	LG:223970.11:2001MAR30	1304	1326	forward 3	TM	Transmembrane
119	LG:223970.11:2001MAR30	1327	1330	forward 3	TM	Cytosolic
119	LG:223970.11:2001MAR30	1331	1353	forward 3	TM	Transmembrane
119	LG:223970.11:2001MAR30	1354	1460	forward 3	TM	Non-Cytosolic
119	LG:223970.11:2001MAR30	1461	1483	forward 3	TM	Transmembrane
119	LG:223970.11:2001MAR30	1484	1495	forward 3	TM	Cytosolic
119	LG:223970.11:2001MAR30	1496	1518	forward 3	TM	Transmembrane
119	LG:223970.11:2001MAR30	1519	1522	forward 3	TM	Non-Cytosolic
119	LG:223970.11:2001MAR30	1523	1545	forward 3	TM	Transmembrane
119	LG:223970.11:2001MAR30	1546	1568	forward 3	TM	Cytosolic
119	LG:223970.11:2001MAR30	1569	1591	forward 3	TM	Transmembrane
119	LG:223970.11:2001MAR30	1592	2022	forward 3	TM	Non-Cytosolic
119	LG:223970.11:2001MAR30	2023	2045	forward 3	TM	Transmembrane
119	LG:223970.11:2001MAR30	2046	2227	forward 3	TM	Cytosolic
119	LG:223970.11:2001MAR30	2228	2250	forward 3	TM	Transmembrane
119	LG:223970.11:2001MAR30	2251	2299	forward 3	TM	Non-Cytosolic
119	LG:223970.11:2001MAR30	2300	2322	forward 3	TM	Transmembrane
119	LG:223970.11:2001MAR30	2323	2341	forward 3	TM	Cytosolic
120	LG:227500.5:2001MAR30	1	855	forward 1	TM	Non-Cytosolic
120	LG:227500.5:2001MAR30	856	875	forward 1	TM	Transmembrane
120	LG:227500.5:2001MAR30	876	1071	forward 1	TM	Cytosolic
120	LG:227500.5:2001MAR30	1072	1094	forward 1	TM	Transmembrane
120	LG:227500.5:2001MAR30	1095	1120	forward 1	TM	Non-Cytosolic
120	LG:227500.5:2001MAR30	1121	1138	forward 1	TM	Transmembrane
120	LG:227500.5:2001MAR30	1139	1152	forward 1	TM	Cytosolic
121	LG:227722.7:2001MAR30	1	249	forward 1	TM	Cytosolic
121	LG:227722.7:2001MAR30	250	272	forward 1	TM	Transmembrane
121	LG:227722.7:2001MAR30	273	628	forward 1	TM	Non-Cytosolic
122	LG:229105.1:2001MAR30	1	184	forward 3	TM	Cytosolic
122	LG:229105.1:2001MAR30	185	207	forward 3	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
122	LG:229105.1:2001MAR30	208	233	forward 3	TM	Non-Cytosolic
122	LG:229105.1:2001MAR30	234	256	forward 3	TM	Transmembrane
122	LG:229105.1:2001MAR30	257	287	forward 3	TM	Cytosolic
122	LG:229105.1:2001MAR30	288	310	forward 3	TM	Transmembrane
122	LG:229105.1:2001MAR30	311	802	forward 3	TM	Non-Cytosolic
123	LG:233761.4:2001MAR30	1	849	forward 1	TM	Non-Cytosolic
123	LG:233761.4:2001MAR30	850	872	forward 1	TM	Transmembrane
123	LG:233761.4:2001MAR30	873	892	forward 1	TM	Cytosolic
123	LG:233761.4:2001MAR30	893	912	forward 1	TM	Transmembrane
123	LG:233761.4:2001MAR30	913	957	forward 1	TM	Non-Cytosolic
123	LG:233761.4:2001MAR30	1	854	forward 2	TM	Non-Cytosolic
123	LG:233761.4:2001MAR30	855	877	forward 2	TM	Transmembrane
123	LG:233761.4:2001MAR30	878	957	forward 2	TM	Cytosolic
123	LG:233761.4:2001MAR30	1	753	forward 3	TM	Non-Cytosolic
123	LG:233761.4:2001MAR30	754	776	forward 3	TM	Transmembrane
123	LG:233761.4:2001MAR30	777	855	forward 3	TM	Cytosolic
123	LG:233761.4:2001MAR30	856	875	forward 3	TM	Transmembrane
123	LG:233761.4:2001MAR30	876	889	forward 3	TM	Non-Cytosolic
123	LG:233761.4:2001MAR30	890	912	forward 3	TM	Transmembrane
123	LG:233761.4:2001MAR30	913	957	forward 3	TM	Cytosolic
124	LG:234326.67:2001MAR30	1	1073	forward 2	TM	Non-Cytosolic
124	LG:234326.67:2001MAR30	1074	1096	forward 2	TM	Transmembrane
124	LG:234326.67:2001MAR30	1097	1173	forward 2	TM	Cytosolic
124	LG:234326.67:2001MAR30	1174	1196	forward 2	TM	Transmembrane
124	LG:234326.67:2001MAR30	1197	1378	forward 2	TM	Non-Cytosolic
124	LG:234326.67:2001MAR30	1379	1401	forward 2	TM	Transmembrane
124	LG:234326.67:2001MAR30	1402	1565	forward 2	TM	Cytosolic
124	LG:234326.67:2001MAR30	1	1133	forward 3	TM	Non-Cytosolic
124	LG:234326.67:2001MAR30	1134	1151	forward 3	TM	Transmembrane
124	LG:234326.67:2001MAR30	1152	1157	forward 3	TM	Cytosolic
124	LG:234326.67:2001MAR30	1158	1180	forward 3	TM	Transmembrane
124	LG:234326.67:2001MAR30	1181	1183	forward 3	TM	Non-Cytosolic
124	LG:234326.67:2001MAR30	1184	1206	forward 3	TM	Transmembrane
124	LG:234326.67:2001MAR30	1207	1249	forward 3	TM	Cytosolic
124	LG:234326.67:2001MAR30	1250	1272	forward 3	TM	Transmembrane
124	LG:234326.67:2001MAR30	1273	1281	forward 3	TM	Non-Cytosolic
124	LG:234326.67:2001MAR30	1282	1304	forward 3	TM	Transmembrane
124	LG:234326.67:2001MAR30	1305	1511	forward 3	TM	Cytosolic
124	LG:234326.67:2001MAR30	1512	1529	forward 3	TM	Transmembrane
124	LG:234326.67:2001MAR30	1530	1533	forward 3	TM	Non-Cytosolic
124	LG:234326.67:2001MAR30	1534	1556	forward 3	TM	Transmembrane
124	LG:234326.67:2001MAR30	1557	1565	forward 3	TM	Cytosolic
125	LG:236056.27:2001MAR30	1	727	forward 1	TM	Non-Cytosolic
125	LG:236056.27:2001MAR30	728	750	forward 1	TM	Transmembrane
125	LG:236056.27:2001MAR30	751	822	forward 1	TM	Cytosolic
125	LG:236056.27:2001MAR30	823	845	forward 1	TM	Transmembrane
125	LG:236056.27:2001MAR30	846	860	forward 1	TM	Non-Cytosolic
125	LG:236056.27:2001MAR30	1	626	forward 3	TM	Non-Cytosolic
125	LG:236056.27:2001MAR30	627	649	forward 3	TM	Transmembrane
125	LG:236056.27:2001MAR30	650	719	forward 3	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
125	LG:236056.27:2001MAR30	720	742	forward 3	TM	Transmembrane
125	LG:236056.27:2001MAR30	743	746	forward 3	TM	Non-Cytosolic
125	LG:236056.27:2001MAR30	747	769	forward 3	TM	Transmembrane
125	LG:236056.27:2001MAR30	770	859	forward 3	TM	Cytosolic
126	LG:253889.31:2001MAR30	1	621	forward 1	TM	Non-Cytosolic
126	LG:253889.31:2001MAR30	622	644	forward 1	TM	Transmembrane
126	LG:253889.31:2001MAR30	645	871	forward 1	TM	Cytosolic
126	LG:253889.31:2001MAR30	872	894	forward 1	TM	Transmembrane
126	LG:253889.31:2001MAR30	895	903	forward 1	TM	Non-Cytosolic
126	LG:253889.31:2001MAR30	904	926	forward 1	TM	Transmembrane
126	LG:253889.31:2001MAR30	927	946	forward 1	TM	Cytosolic
126	LG:253889.31:2001MAR30	947	969	forward 1	TM	Transmembrane
126	LG:253889.31:2001MAR30	970	1284	forward 1	TM	Non-Cytosolic
126	LG:253889.31:2001MAR30	1	574	forward 2	TM	Non-Cytosolic
126	LG:253889.31:2001MAR30	575	597	forward 2	TM	Transmembrane
126	LG:253889.31:2001MAR30	598	865	forward 2	TM	Cytosolic
126	LG:253889.31:2001MAR30	866	888	forward 2	TM	Transmembrane
126	LG:253889.31:2001MAR30	889	946	forward 2	TM	Non-Cytosolic
126	LG:253889.31:2001MAR30	947	969	forward 2	TM	Transmembrane
126	LG:253889.31:2001MAR30	970	1074	forward 2	TM	Cytosolic
126	LG:253889.31:2001MAR30	1075	1097	forward 2	TM	Transmembrane
126	LG:253889.31:2001MAR30	1098	1139	forward 2	TM	Non-Cytosolic
126	LG:253889.31:2001MAR30	1140	1162	forward 2	TM	Transmembrane
126	LG:253889.31:2001MAR30	1163	1221	forward 2	TM	Cytosolic
126	LG:253889.31:2001MAR30	1222	1244	forward 2	TM	Transmembrane
126	LG:253889.31:2001MAR30	1245	1284	forward 2	TM	Non-Cytosolic
126	LG:253889.31:2001MAR30	1	357	forward 3	TM	Non-Cytosolic
126	LG:253889.31:2001MAR30	358	380	forward 3	TM	Transmembrane
126	LG:253889.31:2001MAR30	381	401	forward 3	TM	Cytosolic
126	LG:253889.31:2001MAR30	402	424	forward 3	TM	Transmembrane
126	LG:253889.31:2001MAR30	425	574	forward 3	TM	Non-Cytosolic
126	LG:253889.31:2001MAR30	575	597	forward 3	TM	Transmembrane
126	LG:253889.31:2001MAR30	598	617	forward 3	TM	Cytosolic
126	LG:253889.31:2001MAR30	618	640	forward 3	TM	Transmembrane
126	LG:253889.31:2001MAR30	641	867	forward 3	TM	Non-Cytosolic
126	LG:253889.31:2001MAR30	868	890	forward 3	TM	Transmembrane
126	LG:253889.31:2001MAR30	891	1089	forward 3	TM	Cytosolic
126	LG:253889.31:2001MAR30	1090	1112	forward 3	TM	Transmembrane
126	LG:253889.31:2001MAR30	1113	1126	forward 3	TM	Non-Cytosolic
126	LG:253889.31:2001MAR30	1127	1149	forward 3	TM	Transmembrane
126	LG:253889.31:2001MAR30	1150	1150	forward 3	TM	Cytosolic
126	LG:253889.31:2001MAR30	1151	1173	forward 3	TM	Transmembrane
126	LG:253889.31:2001MAR30	1174	1284	forward 3	TM	Non-Cytosolic
127	LG:270833.135:2001MAR30	1	341	forward 1	TM	Non-Cytosolic
127	LG:270833.135:2001MAR30	342	364	forward 1	TM	Transmembrane
127	LG:270833.135:2001MAR30	365	444	forward 1	TM	Cytosolic
128	LG:292613.7:2001MAR30	1	4	forward 1	TM	Non-Cytosolic
128	LG:292613.7:2001MAR30	5	27	forward 1	TM	Transmembrane
128	LG:292613.7:2001MAR30	28	78	forward 1	TM	Cytosolic
128	LG:292613.7:2001MAR30	79	101	forward 1	TM	Transmembrane



TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
128	LG:292613.7:2001MAR30	102	1272	forward 1	TM	Non-Cytosolic
128	LG:292613.7:2001MAR30	1273	1295	forward 1	TM	Transmembrane
128	LG:292613.7:2001MAR30	1296	1391	forward 1	TM	Cytosolic
128	LG:292613.7:2001MAR30	1392	1414	forward 1	TM	Transmembrane
128	LG:292613.7:2001MAR30	1415	1423	forward 1	TM	Non-Cytosolic
128	LG:292613.7:2001MAR30	1424	1446	forward 1	TM	Transmembrane
128	LG:292613.7:2001MAR30	1447	1514	forward 1	TM	Cytosolic
128	LG:292613.7:2001MAR30	1515	1534	forward 1	TM	Transmembrane
128	LG:292613.7:2001MAR30	1535	1710	forward 1	TM	Non-Cytosolic
128	LG:292613.7:2001MAR30	1	12	forward 2	TM	Cytosolic
128	LG:292613.7:2001MAR30	13	35	forward 2	TM	Transmembrane
128	LG:292613.7:2001MAR30	36	77	forward 2	TM	Non-Cytosolic
128	LG:292613.7:2001MAR30	78	100	forward 2	TM	Transmembrane
128	LG:292613.7:2001MAR30	101	112	forward 2	TM	Cytosolic
128	LG:292613.7:2001MAR30	113	135	forward 2	TM	Transmembrane
128	LG:292613.7:2001MAR30	136	1586	forward 2	TM	Non-Cytosolic
128	LG:292613.7:2001MAR30	1587	1609	forward 2	TM	Transmembrane
128	LG:292613.7:2001MAR30	1610	1628	forward 2	TM	Cytosolic
128	LG:292613.7:2001MAR30	1629	1651	forward 2	TM	Transmembrane
128	LG:292613.7:2001MAR30	1652	1710	forward 2	TM	Non-Cytosolic
128	LG:292613.7:2001MAR30	1	1	forward 3	TM	Cytosolic
128	LG:292613.7:2001MAR30	2	24	forward 3	TM	Transmembrane
128	LG:292613.7:2001MAR30	25	27	forward 3	TM	Non-Cytosolic
128	LG:292613.7:2001MAR30	28	49	forward 3	TM	Transmembrane
128	LG:292613.7:2001MAR30	50	55	forward 3	TM	Cytosolic
128	LG:292613.7:2001MAR30	56	73	forward 3	TM	Transmembrane
128	LG:292613.7:2001MAR30	74	82	forward 3	TM	Non-Cytosolic
128	LG:292613.7:2001MAR30	83	105	forward 3	TM	Transmembrane
128	LG:292613.7:2001MAR30	106	125	forward 3	TM	Cytosolic
128	LG:292613.7:2001MAR30	126	148	forward 3	TM	Transmembrane
128	LG:292613.7:2001MAR30	149	1124	forward 3	TM	Non-Cytosolic
128	LG:292613.7:2001MAR30	1125	1147	forward 3	TM	Transmembrane
128	LG:292613.7:2001MAR30	1148	1167	forward 3	TM	Cytosolic
128	LG:292613.7:2001MAR30	1168	1190	forward 3	TM	Transmembrane
128	LG:292613.7:2001MAR30	1191	1235	forward 3	TM	Non-Cytosolic
128	LG:292613.7:2001MAR30	1236	1258	forward 3	TM	Transmembrane
128	LG:292613.7:2001MAR30	1259	1400	forward 3	TM	Cytosolic
128	LG:292613.7:2001MAR30	1401	1423	forward 3	TM	Transmembrane
128	LG:292613.7:2001MAR30	1424	1467	forward 3	TM	Non-Cytosolic
128	LG:292613.7:2001MAR30	1468	1490	forward 3	TM	Transmembrane
128	LG:292613.7:2001MAR30	1491	1629	forward 3	TM	Cytosolic
128	LG:292613.7:2001MAR30	1630	1652	forward 3	TM	Transmembrane
128	LG:292613.7:2001MAR30	1653	1671	forward 3	TM	Non-Cytosolic
128	LG:292613.7:2001MAR30	1672	1694	forward 3	TM	Transmembrane
128	LG:292613.7:2001MAR30	1695	1709	forward 3	TM	Cytosolic
129	LG:331546.2:2001MAR30	1	1061	forward 1	TM	Non-Cytosolic
129	LG:331546.2:2001MAR30	1062	1079	forward 1	TM	Transmembrane
129	LG:331546.2:2001MAR30	1080	1150	forward 1	TM	Cytosolic
130	LG:332027.6:2001MAR30	1	12	forward 1	TM	Cytosolic
130	LG:332027.6:2001MAR30	13	35	forward 1	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
130	LG:332027.6:2001MAR30	36	112	forward 1	TM	Non-Cytosolic
130	LG:332027.6:2001MAR30	113	135	forward 1	TM	Transmembrane
130	LG:332027.6:2001MAR30	136	147	forward 1	TM	Cytosolic
130	LG:332027.6:2001MAR30	148	170	forward 1	TM	Transmembrane
130	LG:332027.6:2001MAR30	171	700	forward 1	TM	Non-Cytosolic
130	LG:332027.6:2001MAR30	701	723	forward 1	TM	Transmembrane
130	LG:332027.6:2001MAR30	724	743	forward 1	TM	Cytosolic
130	LG:332027.6:2001MAR30	744	766	forward 1	TM	Transmembrane
130	LG:332027.6:2001MAR30	767	785	forward 1	TM	Non-Cytosolic
130	LG:332027.6:2001MAR30	786	808	forward 1	TM	Transmembrane
130	LG:332027.6:2001MAR30	809	995	forward 1	TM	Cytosolic
130	LG:332027.6:2001MAR30	996	1018	forward 1	TM	Transmembrane
130	LG:332027.6:2001MAR30	1019	1098	forward 1	TM	Non-Cytosolic
130	LG:332027.6:2001MAR30	1099	1118	forward 1	TM	Transmembrane
130	LG:332027.6:2001MAR30	1119	1152	forward 1	TM	Cytosolic
130	LG:332027.6:2001MAR30	1	22	forward 2	TM	Non-Cytosolic
130	LG:332027.6:2001MAR30	23	45	forward 2	TM	Transmembrane
130	LG:332027.6:2001MAR30	46	81	forward 2	TM	Cytosolic
130	LG:332027.6:2001MAR30	82	104	forward 2	TM	Transmembrane
130	LG:332027.6:2001MAR30	105	113	forward 2	TM	Non-Cytosolic
130	LG:332027.6:2001MAR30	114	136	forward 2	TM	Transmembrane
130	LG:332027.6:2001MAR30	137	147	forward 2	TM	Cytosolic
130	LG:332027.6:2001MAR30	148	170	forward 2	TM	Transmembrane
130	LG:332027.6:2001MAR30	171	579	forward 2	TM	Non-Cytosolic
130	LG:332027.6:2001MAR30	580	602	forward 2	TM	Transmembrane
130	LG:332027.6:2001MAR30	603	683	forward 2	TM	Cytosolic
130	LG:332027.6:2001MAR30	684	706	forward 2	TM	Transmembrane
130	LG:332027.6:2001MAR30	707	754	forward 2	TM	Non-Cytosolic
130	LG:332027.6:2001MAR30	755	774	forward 2	TM	Transmembrane
130	LG:332027.6:2001MAR30	775	989	forward 2	TM	Cytosolic
130	LG:332027.6:2001MAR30	990	1012	forward 2	TM	Transmembrane
130	LG:332027.6:2001MAR30	1013	1048	forward 2	TM	Non-Cytosolic
130	LG:332027.6:2001MAR30	1049	1071	forward 2	TM	Transmembrane
130	LG:332027.6:2001MAR30	1072	1091	forward 2	TM	Cytosolic
130	LG:332027.6:2001MAR30	1092	1114	forward 2	TM	Transmembrane
130	LG:332027.6:2001MAR30	1115	1151	forward 2	TM	Non-Cytosolic
130	LG:332027.6:2001MAR30	1	49	forward 3	TM	Cytosolic
130	LG:332027.6:2001MAR30	50	72	forward 3	TM	Transmembrane
130	LG:332027.6:2001MAR30	73	880	forward 3	TM	Non-Cytosolic
130	LG:332027.6:2001MAR30	881	903	forward 3	TM	Transmembrane
130	LG:332027.6:2001MAR30	904	930	forward 3	TM	Cytosolic
130	LG:332027.6:2001MAR30	931	953	forward 3	TM	Transmembrane
130	LG:332027.6:2001MAR30	954	1002	forward 3	TM	Non-Cytosolic
130	LG:332027.6:2001MAR30	1003	1025	forward 3	TM	Transmembrane
130	LG:332027.6:2001MAR30	1026	1078	forward 3	TM	Cytosolic
130	LG:332027.6:2001MAR30	1079	1101	forward 3	TM	Transmembrane
130	LG:332027.6:2001MAR30	1102	1151	forward 3	TM	Non-Cytosolic
131	LG:336998.1:2001MAR30	1	714	forward 1	TM	Non-Cytosolic
131	LG:336998.1:2001MAR30	715	737	forward 1	TM	Transmembrane
131	LG:336998.1:2001MAR30	738	831	forward 1	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
131	LG:336998.1:2001MAR30	832	851	forward 1	TM	Transmembrane
131	LG:336998.1:2001MAR30	852	865	forward 1	TM	Non-Cytosolic
131	LG:336998.1:2001MAR30	866	885	forward 1	TM	Transmembrane
131	LG:336998.1:2001MAR30	886	1099	forward 1	TM	Cytosolic
131	LG:336998.1:2001MAR30	1100	1122	forward 1	TM	Transmembrane
131	LG:336998.1:2001MAR30	1123	1363	forward 1	TM	Non-Cytosolic
131	LG:336998.1:2001MAR30	1364	1386	forward 1	TM	Transmembrane
131	LG:336998.1:2001MAR30	1387	1542	forward 1	TM	Cytosolic
131	LG:336998.1:2001MAR30	1543	1565	forward 1	TM	Transmembrane
131	LG:336998.1:2001MAR30	1566	1579	forward 1	TM	Non-Cytosolic
131	LG:336998.1:2001MAR30	1580	1602	forward 1	TM	Transmembrane
131	LG:336998.1:2001MAR30	1603	1804	forward 1	TM	Cytosolic
131	LG:336998.1:2001MAR30	1805	1827	forward 1	TM	Transmembrane
131	LG:336998.1:2001MAR30	1828	5189	forward 1	TM	Non-Cytosolic
131	LG:336998.1:2001MAR30	5190	5212	forward 1	TM	Transmembrane
131	LG:336998.1:2001MAR30	5213	5250	forward 1	TM	Cytosolic
131	LG:336998.1:2001MAR30	5251	5273	forward 1	TM	Transmembrane
131	LG:336998.1:2001MAR30	5274	5282	forward 1	TM	Non-Cytosolic
131	LG:336998.1:2001MAR30	5283	5305	forward 1	TM	Transmembrane
131	LG:336998.1:2001MAR30	5306	5311	forward 1	TM	Cytosolic
131	LG:336998.1:2001MAR30	5312	5334	forward 1	TM	Transmembrane
131	LG:336998.1:2001MAR30	5335	5348	forward 1	TM	Non-Cytosolic
131	LG:336998.1:2001MAR30	5349	5371	forward 1	TM	Transmembrane
131	LG:336998.1:2001MAR30	5372	5444	forward 1	TM	Cytosolic
131	LG:336998.1:2001MAR30	5445	5467	forward 1	TM	Transmembrane
131	LG:336998.1:2001MAR30	5468	5700	forward 1	TM	Non-Cytosolic
131	LG:336998.1:2001MAR30	1	12	forward 2	TM	Cytosolic
131	LG:336998.1:2001MAR30	13	35	forward 2	TM	Transmembrane
131	LG:336998.1:2001MAR30	36	5699	forward 2	TM	Non-Cytosolic
131	LG:336998.1:2001MAR30	1	4342	forward 3	TM	Non-Cytosolic
131	LG:336998.1:2001MAR30	4343	4365	forward 3	TM	Transmembrane
131	LG:336998.1:2001MAR30	4366	4389	forward 3	TM	Cytosolic
131	LG:336998.1:2001MAR30	4390	4412	forward 3	TM	Transmembrane
131	LG:336998.1:2001MAR30	4413	4436	forward 3	TM	Non-Cytosolic
131	LG:336998.1:2001MAR30	4437	4459	forward 3	TM	Transmembrane
131	LG:336998.1:2001MAR30	4460	4724	forward 3	TM	Cytosolic
131	LG:336998.1:2001MAR30	4725	4747	forward 3	TM	Transmembrane
131	LG:336998.1:2001MAR30	4748	5260	forward 3	TM	Non-Cytosolic
131	LG:336998.1:2001MAR30	5261	5283	forward 3	TM	Transmembrane
131	LG:336998.1:2001MAR30	5284	5310	forward 3	TM	Cytosolic
131	LG:336998.1:2001MAR30	5311	5333	forward 3	TM	Transmembrane
131	LG:336998.1:2001MAR30	5334	5352	forward 3	TM	Non-Cytosolic
131	LG:336998.1:2001MAR30	5353	5370	forward 3	TM	Transmembrane
131	LG:336998.1:2001MAR30	5371	5432	forward 3	TM	Cytosolic
131	LG:336998.1:2001MAR30	5433	5455	forward 3	TM	Transmembrane
131	LG:336998.1:2001MAR30	5456	5499	forward 3	TM	Non-Cytosolic
131	LG:336998.1:2001MAR30	5500	5522	forward 3	TM	Transmembrane
131	LG:336998.1:2001MAR30	5523	5699	forward 3	TM	Cytosolic
132	LG:338010.8:2001MAR30	1	102	forward 2	TM	Cytosolic
132	LG:338010.8:2001MAR30	103	125	forward 2	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
132	LG:338010.8:2001MAR30	126	139	forward 2	TM	Non-Cytosolic
132	LG:338010.8:2001MAR30	140	162	forward 2	TM	Transmembrane
132	LG:338010.8:2001MAR30	163	236	forward 2	TM	Cytosolic
132	LG:338010.8:2001MAR30	237	259	forward 2	TM	Transmembrane
132	LG:338010.8:2001MAR30	260	273	forward 2	TM	Non-Cytosolic
132	LG:338010.8:2001MAR30	274	296	forward 2	TM	Transmembrane
132	LG:338010.8:2001MAR30	297	398	forward 2	TM	Cytosolic
132	LG:338010.8:2001MAR30	1	103	forward 3	TM	Cytosolic
132	LG:338010.8:2001MAR30	104	126	forward 3	TM	Transmembrane
132	LG:338010.8:2001MAR30	127	202	forward 3	TM	Non-Cytosolic
132	LG:338010.8:2001MAR30	203	225	forward 3	TM	Transmembrane
132	LG:338010.8:2001MAR30	226	237	forward 3	TM	Cytosolic
132	LG:338010.8:2001MAR30	238	260	forward 3	TM	Transmembrane
132	LG:338010.8:2001MAR30	261	398	forward 3	TM	Non-Cytosolic
133	LG:344597.1:2001MAR30	1	709	forward 1	TM	Non-Cytosolic
133	LG:344597.1:2001MAR30	710	732	forward 1	TM	Transmembrane
133	LG:344597.1:2001MAR30	733	1020	forward 1	TM	Cytosolic
133	LG:344597.1:2001MAR30	1021	1043	forward 1	TM	Transmembrane
133	LG:344597.1:2001MAR30	1044	1696	forward 1	TM	Non-Cytosolic
133	LG:344597.1:2001MAR30	1697	1719	forward 1	TM	Transmembrane
133	LG:344597.1:2001MAR30	1720	1878	forward 1	TM	Cytosolic
133	LG:344597.1:2001MAR30	1	1663	forward 2	TM	Non-Cytosolic
133	LG:344597.1:2001MAR30	1664	1686	forward 2	TM	Transmembrane
133	LG:344597.1:2001MAR30	1687	1698	forward 2	TM	Cytosolic
133	LG:344597.1:2001MAR30	1699	1721	forward 2	TM	Transmembrane
133	LG:344597.1:2001MAR30	1722	1878	forward 2	TM	Non-Cytosolic
134	LG:347361.2:2001MAR30	1	1156	forward 2	TM	Non-Cytosolic
134	LG:347361.2:2001MAR30	1157	1179	forward 2	TM	Transmembrane
134	LG:347361.2:2001MAR30	1180	1344	forward 2	TM	Cytosolic
134	LG:347361.2:2001MAR30	1345	1367	forward 2	TM	Transmembrane
134	LG:347361.2:2001MAR30	1368	2339	forward 2	TM	Non-Cytosolic
134	LG:347361.2:2001MAR30	2340	2362	forward 2	TM	Transmembrane
134	LG:347361.2:2001MAR30	2363	2368	forward 2	TM	Cytosolic
134	LG:347361.2:2001MAR30	2369	2388	forward 2	TM	Transmembrane
134	LG:347361.2:2001MAR30	2389	2438	forward 2	TM	Non-Cytosolic
134	LG:347361.2:2001MAR30	2439	2461	forward 2	TM	Transmembrane
134	LG:347361.2:2001MAR30	2462	2531	forward 2	TM	Cytosolic
134	LG:347361.2:2001MAR30	2532	2554	forward 2	TM	Transmembrane
134	LG:347361.2:2001MAR30	2555	2974	forward 2	TM	Non-Cytosolic
134	LG:347361.2:2001MAR30	1	2517	forward 3	TM	Non-Cytosolic
134	LG:347361.2:2001MAR30	2518	2540	forward 3	TM	Transmembrane
134	LG:347361.2:2001MAR30	2541	2546	forward 3	TM	Cytosolic
134	LG:347361.2:2001MAR30	2547	2564	forward 3	TM	Transmembrane
134	LG:347361.2:2001MAR30	2565	2974	forward 3	TM	Non-Cytosolic
135	LG:349293.17:2001MAR30	1	1028	forward 1	TM	Non-Cytosolic
135	LG:349293.17:2001MAR30	1029	1051	forward 1	TM	Transmembrane
135	LG:349293.17:2001MAR30	1052	1177	forward 1	TM	Cytosolic
135	LG:349293.17:2001MAR30	1178	1200	forward 1	TM	Transmembrane
135	LG:349293.17:2001MAR30	1201	1209	forward 1	TM	Non-Cytosolic
135	LG:349293.17:2001MAR30	1210	1227	forward 1	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
135	LG:349293.17:2001MAR30	1228	1334	forward 1	TM	Cytosolic
135	LG:349293.17:2001MAR30	1	878	forward 2	TM	Non-Cytosolic
135	LG:349293.17:2001MAR30	879	901	forward 2	TM	Transmembrane
135	LG:349293.17:2001MAR30	902	969	forward 2	TM	Cytosolic
135	LG:349293.17:2001MAR30	970	992	forward 2	TM	Transmembrane
135	LG:349293.17:2001MAR30	993	1016	forward 2	TM	Non-Cytosolic
135	LG:349293.17:2001MAR30	1017	1036	forward 2	TM	Transmembrane
135	LG:349293.17:2001MAR30	1037	1040	forward 2	TM	Cytosolic
135	LG:349293.17:2001MAR30	1041	1063	forward 2	TM	Transmembrane
135	LG:349293.17:2001MAR30	1064	1082	forward 2	TM	Non-Cytosolic
135	LG:349293.17:2001MAR30	1083	1105	forward 2	TM	Transmembrane
135	LG:349293.17:2001MAR30	1106	1178	forward 2	TM	Cytosolic
135	LG:349293.17:2001MAR30	1179	1201	forward 2	TM	Transmembrane
135	LG:349293.17:2001MAR30	1202	1334	forward 2	TM	Non-Cytosolic
135	LG:349293.17:2001MAR30	1	803	forward 3	TM	Non-Cytosolic
135	LG:349293.17:2001MAR30	804	823	forward 3	TM	Transmembrane
135	LG:349293.17:2001MAR30	824	887	forward 3	TM	Cytosolic
135	LG:349293.17:2001MAR30	888	907	forward 3	TM	Transmembrane
135	LG:349293.17:2001MAR30	908	961	forward 3	TM	Non-Cytosolic
135	LG:349293.17:2001MAR30	962	984	forward 3	TM	Transmembrane
135	LG:349293.17:2001MAR30	985	1003	forward 3	TM	Cytosolic
135	LG:349293.17:2001MAR30	1004	1023	forward 3	TM	Transmembrane
135	LG:349293.17:2001MAR30	1024	1032	forward 3	TM	Non-Cytosolic
135	LG:349293.17:2001MAR30	1033	1055	forward 3	TM	Transmembrane
135	LG:349293.17:2001MAR30	1056	1088	forward 3	TM	Cytosolic
135	LG:349293.17:2001MAR30	1089	1111	forward 3	TM	Transmembrane
135	LG:349293.17:2001MAR30	1112	1143	forward 3	TM	Non-Cytosolic
135	LG:349293.17:2001MAR30	1144	1166	forward 3	TM	Transmembrane
135	LG:349293.17:2001MAR30	1167	1177	forward 3	TM	Cytosolic
135	LG:349293.17:2001MAR30	1178	1200	forward 3	TM	Transmembrane
135	LG:349293.17:2001MAR30	1201	1334	forward 3	TM	Non-Cytosolic
136	LG:410595.19:2001MAR30	1	621	forward 1	TM	Non-Cytosolic
136	LG:410595.19:2001MAR30	622	644	forward 1	TM	Transmembrane
136	LG:410595.19:2001MAR30	645	656	forward 1	TM	Cytosolic
136	LG:410595.19:2001MAR30	657	679	forward 1	TM	Transmembrane
136	LG:410595.19:2001MAR30	680	736	forward 1	TM	Non-Cytosolic
136	LG:410595.19:2001MAR30	1	622	forward 2	TM	Non-Cytosolic
136	LG:410595.19:2001MAR30	623	645	forward 2	TM	Transmembrane
136	LG:410595.19:2001MAR30	646	651	forward 2	TM	Cytosolic
136	LG:410595.19:2001MAR30	652	674	forward 2	TM	Transmembrane
136	LG:410595.19:2001MAR30	675	736	forward 2	TM	Non-Cytosolic
137	LG:411151.35:2001MAR30	1	1022	forward 1	TM	Non-Cytosolic
137	LG:411151.35:2001MAR30	1023	1045	forward 1	TM	Transmembrane
137	LG:411151.35:2001MAR30	1046	1056	forward 1	TM	Cytosolic
137	LG:411151.35:2001MAR30	1057	1079	forward 1	TM	Transmembrane
137	LG:411151.35:2001MAR30	1080	1093	forward 1	TM	Non-Cytosolic
137	LG:411151.35:2001MAR30	1094	1116	forward 1	TM	Transmembrane
137	LG:411151.35:2001MAR30	1117	1135	forward 1	TM	Cytosolic
137	LG:411151.35:2001MAR30	1136	1158	forward 1	TM	Transmembrane
137	LG:411151.35:2001MAR30	1159	1477	forward 1	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
137	LG:411151.35:2001MAR30	1	1450	forward 2	TM	Non-Cytosolic
137	LG:411151.35:2001MAR30	1451	1473	forward 2	TM	Transmembrane
137	LG:411151.35:2001MAR30	1474	1477	forward 2	TM	Cytosolic
138	LG:411334.8:2001MAR30	1	1300	forward 1	TM	Non-Cytosolic
138	LG:411334.8:2001MAR30	1301	1323	forward 1	TM	Transmembrane
138	LG:411334.8:2001MAR30	1324	1329	forward 1	TM	Cytosolic
138	LG:411334.8:2001MAR30	1330	1352	forward 1	TM	Transmembrane
138	LG:411334.8:2001MAR30	1353	1366	forward 1	TM	Non-Cytosolic
138	LG:411334.8:2001MAR30	1367	1389	forward 1	TM	Transmembrane
138	LG:411334.8:2001MAR30	1390	1395	forward 1	TM	Cytosolic
138	LG:411334.8:2001MAR30	1396	1418	forward 1	TM	Transmembrane
138	LG:411334.8:2001MAR30	1419	1464	forward 1	TM	Non-Cytosolic
138	LG:411334.8:2001MAR30	1465	1487	forward 1	TM	Transmembrane
138	LG:411334.8:2001MAR30	1488	1522	forward 1	TM	Cytosolic
138	LG:411334.8:2001MAR30	1523	1540	forward 1	TM	Transmembrane
138	LG:411334.8:2001MAR30	1541	1639	forward 1	TM	Non-Cytosolic
138	LG:411334.8:2001MAR30	1640	1662	forward 1	TM	Transmembrane
138	LG:411334.8:2001MAR30	1663	1682	forward 1	TM	Cytosolic
138	LG:411334.8:2001MAR30	1683	1700	forward 1	TM	Transmembrane
138	LG:411334.8:2001MAR30	1701	2052	forward 1	TM	Non-Cytosolic
138	LG:411334.8:2001MAR30	2053	2075	forward 1	TM	Transmembrane
138	LG:411334.8:2001MAR30	2076	2189	forward 1	TM	Cytosolic
138	LG:411334.8:2001MAR30	1	1222	forward 2	TM	Non-Cytosolic
138	LG:411334.8:2001MAR30	1223	1245	forward 2	TM	Transmembrane
138	LG:411334.8:2001MAR30	1246	1251	forward 2	TM	Cytosolic
138	LG:411334.8:2001MAR30	1252	1274	forward 2	TM	Transmembrane
138	LG:411334.8:2001MAR30	1275	1297	forward 2	TM	Non-Cytosolic
138	LG:411334.8:2001MAR30	1298	1320	forward 2	TM	Transmembrane
138	LG:411334.8:2001MAR30	1321	1566	forward 2	TM	Cytosolic
138	LG:411334.8:2001MAR30	1567	1589	forward 2	TM	Transmembrane
138	LG:411334.8:2001MAR30	1590	1603	forward 2	TM	Non-Cytosolic
138	LG:411334.8:2001MAR30	1604	1626	forward 2	TM	Transmembrane
138	LG:411334.8:2001MAR30	1627	1638	forward 2	TM	Cytosolic
138	LG:411334.8:2001MAR30	1639	1661	forward 2	TM	Transmembrane
138	LG:411334.8:2001MAR30	1662	2188	forward 2	TM	Non-Cytosolic
138	LG:411334.8:2001MAR30	1	848	forward 3	TM	Non-Cytosolic
138	LG:411334.8:2001MAR30	849	871	forward 3	TM	Transmembrane
138	LG:411334.8:2001MAR30	872	1343	forward 3	TM	Cytosolic
138	LG:411334.8:2001MAR30	1344	1366	forward 3	TM	Transmembrane
138	LG:411334.8:2001MAR30	1367	1399	forward 3	TM	Non-Cytosolic
138	LG:411334.8:2001MAR30	1400	1422	forward 3	TM	Transmembrane
138	LG:411334.8:2001MAR30	1423	1522	forward 3	TM	Cytosolic
138	LG:411334.8:2001MAR30	1523	1545	forward 3	TM	Transmembrane
138	LG:411334.8:2001MAR30	1546	1604	forward 3	TM	Non-Cytosolic
138	LG:411334.8:2001MAR30	1605	1627	forward 3	TM	Transmembrane
138	LG:411334.8:2001MAR30	1628	1639	forward 3	TM	Cytosolic
138	LG:411334.8:2001MAR30	1640	1659	forward 3	TM	Transmembrane
138	LG:411334.8:2001MAR30	1660	1683	forward 3	TM	Non-Cytosolic
138	LG:411334.8:2001MAR30	1684	1706	forward 3	TM	Transmembrane
138	LG:411334.8:2001MAR30	1707	1717	forward 3	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
138	LG:411334.8:2001MAR30	1718	1737	forward 3	TM	Transmembrane
138	LG:411334.8:2001MAR30	1738	2188	forward 3	TM	Non-Cytosolic
139	LG:458583.1:2001MAR30	1	108	forward 2	TM	Cytosolic
139	LG:458583.1:2001MAR30	109	131	forward 2	TM	Transmembrane
139	LG:458583.1:2001MAR30	132	238	forward 2	TM	Non-Cytosolic
140	LG:475378.1:2001MAR30	1	1018	forward 2	TM	Non-Cytosolic
140	LG:475378.1:2001MAR30	1019	1041	forward 2	TM	Transmembrane
140	LG:475378.1:2001MAR30	1042	1230	forward 2	TM	Cytosolic
140	LG:475378.1:2001MAR30	1231	1253	forward 2	TM	Transmembrane
140	LG:475378.1:2001MAR30	1254	1267	forward 2	TM	Non-Cytosolic
140	LG:475378.1:2001MAR30	1268	1290	forward 2	TM	Transmembrane
140	LG:475378.1:2001MAR30	1291	1310	forward 2	TM	Cytosolic
140	LG:475378.1:2001MAR30	1311	1333	forward 2	TM	Transmembrane
140	LG:475378.1:2001MAR30	1334	1378	forward 2	TM	Non-Cytosolic
140	LG:475378.1:2001MAR30	1379	1401	forward 2	TM	Transmembrane
140	LG:475378.1:2001MAR30	1402	1413	forward 2	TM	Cytosolic
140	LG:475378.1:2001MAR30	1414	1436	forward 2	TM	Transmembrane
140	LG:475378.1:2001MAR30	1437	1449	forward 2	TM	Non-Cytosolic
141	LG:481572.1:2001MAR30	1	1131	forward 1	TM	Non-Cytosolic
141	LG:481572.1:2001MAR30	1132	1154	forward 1	TM	Transmembrane
141	LG:481572.1:2001MAR30	1155	1185	forward 1	TM	Cytosolic
141	LG:481572.1:2001MAR30	1186	1208	forward 1	TM	Transmembrane
141	LG:481572.1:2001MAR30	1209	1212	forward 1	TM	Non-Cytosolic
141	LG:481572.1:2001MAR30	1213	1235	forward 1	TM	Transmembrane
141	LG:481572.1:2001MAR30	1236	1241	forward 1	TM	Cytosolic
141	LG:481572.1:2001MAR30	1242	1264	forward 1	TM	Transmembrane
141	LG:481572.1:2001MAR30	1265	1725	forward 1	TM	Non-Cytosolic
141	LG:481572.1:2001MAR30	1	1185	forward 2	TM	Non-Cytosolic
141	LG:481572.1:2001MAR30	1186	1208	forward 2	TM	Transmembrane
141	LG:481572.1:2001MAR30	1209	1212	forward 2	TM	Cytosolic
141	LG:481572.1:2001MAR30	1213	1232	forward 2	TM	Transmembrane
141	LG:481572.1:2001MAR30	1233	1725	forward 2	TM	Non-Cytosolic
142	LG:481704.1:2001MAR30	1	342	forward 1	TM	Non-Cytosolic
142	LG:481704.1:2001MAR30	343	365	forward 1	TM	Transmembrane
142	LG:481704.1:2001MAR30	366	411	forward 1	TM	Cytosolic
142	LG:481704.1:2001MAR30	412	434	forward 1	TM	Transmembrane
142	LG:481704.1:2001MAR30	435	448	forward 1	TM	Non-Cytosolic
142	LG:481704.1:2001MAR30	449	471	forward 1	TM	Transmembrane
142	LG:481704.1:2001MAR30	472	526	forward 1	TM	Cytosolic
142	LG:481704.1:2001MAR30	1	433	forward 2	TM	Non-Cytosolic
142	LG:481704.1:2001MAR30	434	456	forward 2	TM	Transmembrane
142	LG:481704.1:2001MAR30	457	462	forward 2	TM	Cytosolic
142	LG:481704.1:2001MAR30	463	485	forward 2	TM	Transmembrane
142	LG:481704.1:2001MAR30	486	525	forward 2	TM	Non-Cytosolic
142	LG:481704.1:2001MAR30	1	457	forward 3	TM	Non-Cytosolic
142	LG:481704.1:2001MAR30	458	480	forward 3	TM	Transmembrane
142	LG:481704.1:2001MAR30	481	500	forward 3	TM	Cytosolic
142	LG:481704.1:2001MAR30	501	523	forward 3	TM	Transmembrane
142	LG:481704.1:2001MAR30	524	525	forward 3	TM	Non-Cytosolic
143	LG:898195.4:2001MAR30	1	739	forward 1	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
143	LG:898195.4:2001MAR30	740	759	forward 1	TM	Transmembrane
143	LG:898195.4:2001MAR30	760	876	forward 1	TM	Cytosolic
143	LG:898195.4:2001MAR30	877	899	forward 1	TM	Transmembrane
143	LG:898195.4:2001MAR30	900	1162	forward 1	TM	Non-Cytosolic
143	LG:898195.4:2001MAR30	1163	1185	forward 1	TM	Transmembrane
143	LG:898195.4:2001MAR30	1186	1205	forward 1	TM	Cytosolic
143	LG:898195.4:2001MAR30	1	738	forward 2	TM	Non-Cytosolic
143	LG:898195.4:2001MAR30	739	761	forward 2	TM	Transmembrane
143	LG:898195.4:2001MAR30	762	878	forward 2	TM	Cytosolic
143	LG:898195.4:2001MAR30	879	901	forward 2	TM	Transmembrane
143	LG:898195.4:2001MAR30	902	1020	forward 2	TM	Non-Cytosolic
143	LG:898195.4:2001MAR30	1021	1043	forward 2	TM	Transmembrane
143	LG:898195.4:2001MAR30	1044	1130	forward 2	TM	Cytosolic
143	LG:898195.4:2001MAR30	1131	1153	forward 2	TM	Transmembrane
143	LG:898195.4:2001MAR30	1154	1162	forward 2	TM	Non-Cytosolic
143	LG:898195.4:2001MAR30	1163	1185	forward 2	TM	Transmembrane
143	LG:898195.4:2001MAR30	1186	1204	forward 2	TM	Cytosolic
143	LG:898195.4:2001MAR30	1	516	forward 3	TM	Non-Cytosolic
143	LG:898195.4:2001MAR30	517	539	forward 3	TM	Transmembrane
143	LG:898195.4:2001MAR30	540	637	forward 3	TM	Cytosolic
143	LG:898195.4:2001MAR30	638	660	forward 3	TM	Transmembrane
143	LG:898195.4:2001MAR30	661	738	forward 3	TM	Non-Cytosolic
143	LG:898195.4:2001MAR30	739	761	forward 3	TM	Transmembrane
143	LG:898195.4:2001MAR30	762	780	forward 3	TM	Cytosolic
143	LG:898195.4:2001MAR30	781	803	forward 3	TM	Transmembrane
143	LG:898195.4:2001MAR30	804	874	forward 3	TM	Non-Cytosolic
143	LG:898195.4:2001MAR30	875	897	forward 3	TM	Transmembrane
143	LG:898195.4:2001MAR30	898	1016	forward 3	TM	Cytosolic
143	LG:898195.4:2001MAR30	1017	1039	forward 3	TM	Transmembrane
143	LG:898195.4:2001MAR30	1040	1058	forward 3	TM	Non-Cytosolic
143	LG:898195.4:2001MAR30	1059	1081	forward 3	TM	Transmembrane
143	LG:898195.4:2001MAR30	1082	1089	forward 3	TM	Cytosolic
143	LG:898195.4:2001MAR30	1090	1112	forward 3	TM	Transmembrane
143	LG:898195.4:2001MAR30	1113	1131	forward 3	TM	Non-Cytosolic
143	LG:898195.4:2001MAR30	1132	1154	forward 3	TM	Transmembrane
143	LG:898195.4:2001MAR30	1155	1160	forward 3	TM	Cytosolic
143	LG:898195.4:2001MAR30	1161	1183	forward 3	TM	Transmembrane
143	LG:898195.4:2001MAR30	1184	1204	forward 3	TM	Non-Cytosolic
144	LG:903785.1:2001MAR30	1	1456	forward 2	TM	Non-Cytosolic
144	LG:903785.1:2001MAR30	1457	1479	forward 2	TM	Transmembrane
144	LG:903785.1:2001MAR30	1480	1483	forward 2	TM	Cytosolic
144	LG:903785.1:2001MAR30	1484	1501	forward 2	TM	Transmembrane
144	LG:903785.1:2001MAR30	1502	1541	forward 2	TM	Non-Cytosolic
144	LG:903785.1:2001MAR30	1542	1564	forward 2	TM	Transmembrane
144	LG:903785.1:2001MAR30	1565	1570	forward 2	TM	Cytosolic
144	LG:903785.1:2001MAR30	1571	1593	forward 2	TM	Transmembrane
144	LG:903785.1:2001MAR30	1594	1602	forward 2	TM	Non-Cytosolic
144	LG:903785.1:2001MAR30	1603	1620	forward 2	TM	Transmembrane
144	LG:903785.1:2001MAR30	1621	1676	forward 2	TM	Cytosolic
145	LG:977454.3:2001MAR30	1	344	forward 1	TM	Non-Cytosolic



TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
145	LG:977454.3:2001MAR30	345	367	forward 1	TM	Transmembrane
145	LG:977454.3:2001MAR30	368	387	forward 1	TM	Cytosolic
145	LG:977454.3:2001MAR30	388	407	forward 1	TM	Transmembrane
145	LG:977454.3:2001MAR30	408	1017	forward 1	TM	Non-Cytosolic
145	LG:977454.3:2001MAR30	1	216	forward 2	TM	Non-Cytosolic
145	LG:977454.3:2001MAR30	217	239	forward 2	TM	Transmembrane
145	LG:977454.3:2001MAR30	240	334	forward 2	TM	Cytosolic
145	LG:977454.3:2001MAR30	335	357	forward 2	TM	Transmembrane
145	LG:977454.3:2001MAR30	358	360	forward 2	TM	Non-Cytosolic
145	LG:977454.3:2001MAR30	361	383	forward 2	TM	Transmembrane
145	LG:977454.3:2001MAR30	384	395	forward 2	TM	Cytosolic
145	LG:977454.3:2001MAR30	396	418	forward 2	TM	Transmembrane
145	LG:977454.3:2001MAR30	419	1017	forward 2	TM	Non-Cytosolic
146	LG:977724.12:2001MAR30	1	1131	forward 1	TM	Non-Cytosolic
146	LG:977724.12:2001MAR30	1132	1154	forward 1	TM	Transmembrane
146	LG:977724.12:2001MAR30	1155	1635	forward 1	TM	Cytosolic
146	LG:977724.12:2001MAR30	1636	1658	forward 1	TM	Transmembrane
146	LG:977724.12:2001MAR30	1659	1667	forward 1	TM	Non-Cytosolic
146	LG:977724.12:2001MAR30	1668	1685	forward 1	TM	Transmembrane
146	LG:977724.12:2001MAR30	1686	1735	forward 1	TM	Cytosolic
146	LG:977724.12:2001MAR30	1	1144	forward 2	TM	Non-Cytosolic
146	LG:977724.12:2001MAR30	1145	1167	forward 2	TM	Transmembrane
146	LG:977724.12:2001MAR30	1168	1636	forward 2	TM	Cytosolic
146	LG:977724.12:2001MAR30	1637	1659	forward 2	TM	Transmembrane
146	LG:977724.12:2001MAR30	1660	1662	forward 2	TM	Non-Cytosolic
146	LG:977724.12:2001MAR30	1663	1685	forward 2	TM	Transmembrane
146	LG:977724.12:2001MAR30	1686	1734	forward 2	TM	Cytosolic
146	LG:977724.12:2001MAR30	1	1598	forward 3	TM	Non-Cytosolic
146	LG:977724.12:2001MAR30	1599	1621	forward 3	TM	Transmembrane
146	LG:977724.12:2001MAR30	1622	1669	forward 3	TM	Cytosolic
146	LG:977724.12:2001MAR30	1670	1687	forward 3	TM	Transmembrane
146	LG:977724.12:2001MAR30	1688	1696	forward 3	TM	Non-Cytosolic
146	LG:977724.12:2001MAR30	1697	1719	forward 3	TM	Transmembrane
146	LG:977724.12:2001MAR30	1720	1734	forward 3	TM	Cytosolic
147	LG:978215.19:2001MAR30	1	57	forward 3	TM	Cytosolic
147	LG:978215.19:2001MAR30	58	80	forward 3	TM	Transmembrane
147	LG:978215.19:2001MAR30	81	909	forward 3	TM	Non-Cytosolic
148	LG:981795.1:2001MAR30	1	19	forward 1	TM	Non-Cytosolic
148	LG:981795.1:2001MAR30	20	42	forward 1	TM	Transmembrane
148	LG:981795.1:2001MAR30	43	95	forward 1	TM	Cytosolic
148	LG:981795.1:2001MAR30	96	118	forward 1	TM	Transmembrane
148	LG:981795.1:2001MAR30	119	166	forward 1	TM	Non-Cytosolic
148	LG:981795.1:2001MAR30	167	189	forward 1	TM	Transmembrane
148	LG:981795.1:2001MAR30	190	209	forward 1	TM	Cytosolic
148	LG:981795.1:2001MAR30	210	232	forward 1	TM	Transmembrane
148	LG:981795.1:2001MAR30	233	259	forward 1	TM	Non-Cytosolic
148	LG:981795.1:2001MAR30	260	282	forward 1	TM	Transmembrane
148	LG:981795.1:2001MAR30	283	457	forward 1	TM	Cytosolic
148	LG:981795.1:2001MAR30	458	480	forward 1	TM	Transmembrane
148	LG:981795.1:2001MAR30	481	798	forward 1	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
148	LG:981795.1:2001MAR30	1	74	forward 2	TM	Cytosolic
148	LG:981795.1:2001MAR30	75	97	forward 2	TM	Transmembrane
148	LG:981795.1:2001MAR30	98	106	forward 2	TM	Non-Cytosolic
148	LG:981795.1:2001MAR30	107	129	forward 2	TM	Transmembrane
148	LG:981795.1:2001MAR30	130	224	forward 2	TM	Cytosolic
148	LG:981795.1:2001MAR30	225	247	forward 2	TM	Transmembrane
148	LG:981795.1:2001MAR30	248	261	forward 2	TM	Non-Cytosolic
148	LG:981795.1:2001MAR30	262	282	forward 2	TM	Transmembrane
148	LG:981795.1:2001MAR30	283	372	forward 2	TM	Cytosolic
148	LG:981795.1:2001MAR30	373	395	forward 2	TM	Transmembrane
148	LG:981795.1:2001MAR30	396	414	forward 2	TM	Non-Cytosolic
148	LG:981795.1:2001MAR30	415	437	forward 2	TM	Transmembrane
148	LG:981795.1:2001MAR30	438	798	forward 2	TM	Cytosolic
148	LG:981795.1:2001MAR30	1	4	forward 3	TM	Non-Cytosolic
148	LG:981795.1:2001MAR30	5	22	forward 3	TM	Transmembrane
148	LG:981795.1:2001MAR30	23	224	forward 3	TM	Cytosolic
148	LG:981795.1:2001MAR30	225	247	forward 3	TM	Transmembrane
148	LG:981795.1:2001MAR30	248	261	forward 3	TM	Non-Cytosolic
148	LG:981795.1:2001MAR30	262	281	forward 3	TM	Transmembrane
148	LG:981795.1:2001MAR30	282	372	forward 3	TM	Cytosolic
148	LG:981795.1:2001MAR30	373	395	forward 3	TM	Transmembrane
148	LG:981795.1:2001MAR30	396	456	forward 3	TM	Non-Cytosolic
148	LG:981795.1:2001MAR30	457	479	forward 3	TM	Transmembrane
148	LG:981795.1:2001MAR30	480	536	forward 3	TM	Cytosolic
148	LG:981795.1:2001MAR30	537	559	forward 3	TM	Transmembrane
148	LG:981795.1:2001MAR30	560	797	forward 3	TM	Non-Cytosolic
149	LG:982784.1:2001MAR30	1	315	forward 1	TM	Non-Cytosolic
149	LG:982784.1:2001MAR30	316	338	forward 1	TM	Transmembrane
149	LG:982784.1:2001MAR30	339	358	forward 1	TM	Cytosolic
149	LG:982784.1:2001MAR30	359	381	forward 1	TM	Transmembrane
149	LG:982784.1:2001MAR30	382	491	forward 1	TM	Non-Cytosolic
149	LG:982784.1:2001MAR30	1	359	forward 2	TM	Non-Cytosolic
149	LG:982784.1:2001MAR30	360	382	forward 2	TM	Transmembrane
149	LG:982784.1:2001MAR30	383	490	forward 2	TM	Cytosolic
149	LG:982784.1:2001MAR30	1	227	forward 3	TM	Cytosolic
149	LG:982784.1:2001MAR30	228	246	forward 3	TM	Transmembrane
149	LG:982784.1:2001MAR30	247	255	forward 3	TM	Non-Cytosolic
149	LG:982784.1:2001MAR30	256	278	forward 3	TM	Transmembrane
149	LG:982784.1:2001MAR30	279	490	forward 3	TM	Cytosolic
150	LG:987322.4:2001MAR30	1	820	forward 1	TM	Non-Cytosolic
150	LG:987322.4:2001MAR30	821	843	forward 1	TM	Transmembrane
150	LG:987322.4:2001MAR30	844	862	forward 1	TM	Cytosolic
150	LG:987322.4:2001MAR30	863	885	forward 1	TM	Transmembrane
150	LG:987322.4:2001MAR30	886	1048	forward 1	TM	Non-Cytosolic
150	LG:987322.4:2001MAR30	1049	1071	forward 1	TM	Transmembrane
150	LG:987322.4:2001MAR30	1072	1223	forward 1	TM	Cytosolic
150	LG:987322.4:2001MAR30	1224	1246	forward 1	TM	Transmembrane
150	LG:987322.4:2001MAR30	1247	1277	forward 1	TM	Non-Cytosolic
150	LG:987322.4:2001MAR30	1278	1300	forward 1	TM	Transmembrane
150	LG:987322.4:2001MAR30	1301	1320	forward 1	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
150	LG:987322.4:2001MAR30	1321	1343	forward 1	TM	Transmembrane
150	LG:987322.4:2001MAR30	1344	1352	forward 1	TM	Non-Cytosolic
150	LG:987322.4:2001MAR30	1353	1372	forward 1	TM	Transmembrane
150	LG:987322.4:2001MAR30	1373	1374	forward 1	TM	Cytosolic
150	LG:987322.4:2001MAR30	1	826	forward 2	TM	Non-Cytosolic
150	LG:987322.4:2001MAR30	827	845	forward 2	TM	Transmembrane
150	LG:987322.4:2001MAR30	846	865	forward 2	TM	Cytosolic
150	LG:987322.4:2001MAR30	866	888	forward 2	TM	Transmembrane
150	LG:987322.4:2001MAR30	889	995	forward 2	TM	Non-Cytosolic
150	LG:987322.4:2001MAR30	996	1018	forward 2	TM	Transmembrane
150	LG:987322.4:2001MAR30	1019	1030	forward 2	TM	Cytosolic
150	LG:987322.4:2001MAR30	1031	1053	forward 2	TM	Transmembrane
150	LG:987322.4:2001MAR30	1054	1083	forward 2	TM	Non-Cytosolic
150	LG:987322.4:2001MAR30	1084	1103	forward 2	TM	Transmembrane
150	LG:987322.4:2001MAR30	1104	1313	forward 2	TM	Cytosolic
150	LG:987322.4:2001MAR30	1314	1333	forward 2	TM	Transmembrane
150	LG:987322.4:2001MAR30	1334	1352	forward 2	TM	Non-Cytosolic
150	LG:987322.4:2001MAR30	1353	1372	forward 2	TM	Transmembrane
150	LG:987322.4:2001MAR30	1373	1373	forward 2	TM	Cytosolic
150	LG:987322.4:2001MAR30	1	507	forward 3	TM	Non-Cytosolic
150	LG:987322.4:2001MAR30	508	530	forward 3	TM	Transmembrane
150	LG:987322.4:2001MAR30	531	659	forward 3	TM	Cytosolic
150	LG:987322.4:2001MAR30	660	682	forward 3	TM	Transmembrane
150	LG:987322.4:2001MAR30	683	691	forward 3	TM	Non-Cytosolic
150	LG:987322.4:2001MAR30	692	709	forward 3	TM	Transmembrane
150	LG:987322.4:2001MAR30	710	812	forward 3	TM	Cytosolic
150	LG:987322.4:2001MAR30	813	835	forward 3	TM	Transmembrane
150	LG:987322.4:2001MAR30	836	1373	forward 3	TM	Non-Cytosolic
151	LG:006242.7:2001MAR30	1	608	forward 2	TM	Non-Cytosolic
151	LG:006242.7:2001MAR30	609	631	forward 2	TM	Transmembrane
151	LG:006242.7:2001MAR30	632	744	forward 2	TM	Cytosolic
151	LG:006242.7:2001MAR30	1	585	forward 3	TM	Non-Cytosolic
151	LG:006242.7:2001MAR30	586	608	forward 3	TM	Transmembrane
151	LG:006242.7:2001MAR30	609	628	forward 3	TM	Cytosolic
151	LG:006242.7:2001MAR30	629	651	forward 3	TM	Transmembrane
151	LG:006242.7:2001MAR30	652	744	forward 3	TM	Non-Cytosolic
152	LG:027320.7:2001MAR30	1	194	forward 2	TM	Cytosolic
152	LG:027320.7:2001MAR30	195	217	forward 2	TM	Transmembrane
152	LG:027320.7:2001MAR30	218	236	forward 2	TM	Non-Cytosolic
152	LG:027320.7:2001MAR30	237	259	forward 2	TM	Transmembrane
152	LG:027320.7:2001MAR30	260	375	forward 2	TM	Cytosolic
152	LG:027320.7:2001MAR30	376	398	forward 2	TM	Transmembrane
152	LG:027320.7:2001MAR30	399	425	forward 2	TM	Non-Cytosolic
152	LG:027320.7:2001MAR30	426	448	forward 2	TM	Transmembrane
152	LG:027320.7:2001MAR30	449	460	forward 2	TM	Cytosolic
152	LG:027320.7:2001MAR30	461	483	forward 2	TM	Transmembrane
152	LG:027320.7:2001MAR30	484	486	forward 2	TM	Non-Cytosolic
152	LG:027320.7:2001MAR30	1	194	forward 3	TM	Cytosolic
152	LG:027320.7:2001MAR30	195	217	forward 3	TM	Transmembrane
152	LG:027320.7:2001MAR30	218	248	forward 3	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
152	LG:027320.7:2001MAR30	249	264	forward 3	TM	Transmembrane
152	LG:027320.7:2001MAR30	265	276	forward 3	TM	Cytosolic
152	LG:027320.7:2001MAR30	277	299	forward 3	TM	Transmembrane
152	LG:027320.7:2001MAR30	300	318	forward 3	TM	Non-Cytosolic
152	LG:027320.7:2001MAR30	319	341	forward 3	TM	Transmembrane
152	LG:027320.7:2001MAR30	342	361	forward 3	TM	Cytosolic
152	LG:027320.7:2001MAR30	362	384	forward 3	TM	Transmembrane
152	LG:027320.7:2001MAR30	385	387	forward 3	TM	Non-Cytosolic
152	LG:027320.7:2001MAR30	388	410	forward 3	TM	Transmembrane
152	LG:027320.7:2001MAR30	411	485	forward 3	TM	Cytosolic
153	LG:147541.44:2001MAR30	1	373	forward 1	TM	Non-Cytosolic
153	LG:147541.44:2001MAR30	374	396	forward 1	TM	Transmembrane
153	LG:147541.44:2001MAR30	397	407	forward 1	TM	Cytosolic
153	LG:147541.44:2001MAR30	408	430	forward 1	TM	Transmembrane
153	LG:147541.44:2001MAR30	431	497	forward 1	TM	Non-Cytosolic
153	LG:147541.44:2001MAR30	498	520	forward 1	TM	Transmembrane
153	LG:147541.44:2001MAR30	521	570	forward 1	TM	Cytosolic
153	LG:147541.44:2001MAR30	571	593	forward 1	TM	Transmembrane
153	LG:147541.44:2001MAR30	594	940	forward 1	TM	Non-Cytosolic
153	LG:147541.44:2001MAR30	941	963	forward 1	TM	Transmembrane
153	LG:147541.44:2001MAR30	964	971	forward 1	TM	Cytosolic
153	LG:147541.44:2001MAR30	972	994	forward 1	TM	Transmembrane
153	LG:147541.44:2001MAR30	995	1218	forward 1	TM	Non-Cytosolic
153	LG:147541.44:2001MAR30	1	364	forward 2	TM	Non-Cytosolic
153	LG:147541.44:2001MAR30	365	387	forward 2	TM	Transmembrane
153	LG:147541.44:2001MAR30	388	399	forward 2	TM	Cytosolic
153	LG:147541.44:2001MAR30	400	419	forward 2	TM	Transmembrane
153	LG:147541.44:2001MAR30	420	802	forward 2	TM	Non-Cytosolic
153	LG:147541.44:2001MAR30	803	820	forward 2	TM	Transmembrane
153	LG:147541.44:2001MAR30	821	852	forward 2	TM	Cytosolic
153	LG:147541.44:2001MAR30	853	872	forward 2	TM	Transmembrane
153	LG:147541.44:2001MAR30	873	886	forward 2	TM	Non-Cytosolic
153	LG:147541.44:2001MAR30	887	901	forward 2	TM	Transmembrane
153	LG:147541.44:2001MAR30	902	920	forward 2	TM	Cytosolic
153	LG:147541.44:2001MAR30	921	943	forward 2	TM	Transmembrane
153	LG:147541.44:2001MAR30	944	962	forward 2	TM	Non-Cytosolic
153	LG:147541.44:2001MAR30	963	985	forward 2	TM	Transmembrane
153	LG:147541.44:2001MAR30	986	1047	forward 2	TM	Cytosolic
153	LG:147541.44:2001MAR30	1048	1070	forward 2	TM	Transmembrane
153	LG:147541.44:2001MAR30	1071	1084	forward 2	TM	Non-Cytosolic
153	LG:147541.44:2001MAR30	1085	1103	forward 2	TM	Transmembrane
153	LG:147541.44:2001MAR30	1104	1109	forward 2	TM	Cytosolic
153	LG:147541.44:2001MAR30	1110	1132	forward 2	TM	Transmembrane
153	LG:147541.44:2001MAR30	1133	1146	forward 2	TM	Non-Cytosolic
153	LG:147541.44:2001MAR30	1147	1169	forward 2	TM	Transmembrane
153	LG:147541.44:2001MAR30	1170	1189	forward 2	TM	Cytosolic
153	LG:147541.44:2001MAR30	1190	1212	forward 2	TM	Transmembrane
153	LG:147541.44:2001MAR30	1213	1217	forward 2	TM	Non-Cytosolic
153	LG:147541.44:2001MAR30	1	71	forward 3	TM	Non-Cytosolic
153	LG:147541.44:2001MAR30	72	94	forward 3	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
153	LG:147541.44:2001MAR30	95	351	forward 3	TM	Cytosolic
153	LG:147541.44:2001MAR30	352	369	forward 3	TM	Transmembrane
153	LG:147541.44:2001MAR30	370	372	forward 3	TM	Non-Cytosolic
153	LG:147541.44:2001MAR30	373	390	forward 3	TM	Transmembrane
153	LG:147541.44:2001MAR30	391	497	forward 3	TM	Cytosolic
153	LG:147541.44:2001MAR30	498	520	forward 3	TM	Transmembrane
153	LG:147541.44:2001MAR30	521	1217	forward 3	TM	Non-Cytosolic
154	LG:228319.2:2001MAR30	1	305	forward 2	TM	Non-Cytosolic
154	LG:228319.2:2001MAR30	306	328	forward 2	TM	Transmembrane
154	LG:228319.2:2001MAR30	329	410	forward 2	TM	Cytosolic
154	LG:228319.2:2001MAR30	411	433	forward 2	TM	Transmembrane
154	LG:228319.2:2001MAR30	434	461	forward 2	TM	Non-Cytosolic
155	LG:238754.19:2001MAR30	1	275	forward 1	TM	Cytosolic
155	LG:238754.19:2001MAR30	276	298	forward 1	TM	Transmembrane
155	LG:238754.19:2001MAR30	299	764	forward 1	TM	Non-Cytosolic
155	LG:238754.19:2001MAR30	1	274	forward 3	TM	Cytosolic
155	LG:238754.19:2001MAR30	275	297	forward 3	TM	Transmembrane
155	LG:238754.19:2001MAR30	298	306	forward 3	TM	Non-Cytosolic
155	LG:238754.19:2001MAR30	307	329	forward 3	TM	Transmembrane
155	LG:238754.19:2001MAR30	330	419	forward 3	TM	Cytosolic
155	LG:238754.19:2001MAR30	420	439	forward 3	TM	Transmembrane
155	LG:238754.19:2001MAR30	440	763	forward 3	TM	Non-Cytosolic
156	LG:405751.12:2001MAR30	1	581	forward 1	TM	Non-Cytosolic
156	LG:405751.12:2001MAR30	582	604	forward 1	TM	Transmembrane
156	LG:405751.12:2001MAR30	605	777	forward 1	TM	Cytosolic
156	LG:405751.12:2001MAR30	778	797	forward 1	TM	Transmembrane
156	LG:405751.12:2001MAR30	798	937	forward 1	TM	Non-Cytosolic
156	LG:405751.12:2001MAR30	1	580	forward 2	TM	Non-Cytosolic
156	LG:405751.12:2001MAR30	581	603	forward 2	TM	Transmembrane
156	LG:405751.12:2001MAR30	604	632	forward 2	TM	Cytosolic
156	LG:405751.12:2001MAR30	633	655	forward 2	TM	Transmembrane
156	LG:405751.12:2001MAR30	656	936	forward 2	TM	Non-Cytosolic
156	LG:405751.12:2001MAR30	1	98	forward 3	TM	Cytosolic
156	LG:405751.12:2001MAR30	99	118	forward 3	TM	Transmembrane
156	LG:405751.12:2001MAR30	119	936	forward 3	TM	Non-Cytosolic
237	LI:018494.1:2001MAY17	1	4	forward 1	TM	Cytosolic
237	LI:018494.1:2001MAY17	5	27	forward 1	TM	Transmembrane
237	LI:018494.1:2001MAY17	28	36	forward 1	TM	Non-Cytosolic
237	LI:018494.1:2001MAY17	37	59	forward 1	TM	Transmembrane
237	LI:018494.1:2001MAY17	60	79	forward 1	TM	Cytosolic
237	LI:018494.1:2001MAY17	80	102	forward 1	TM	Transmembrane
237	LI:018494.1:2001MAY17	103	116	forward 1	TM	Non-Cytosolic
237	LI:018494.1:2001MAY17	117	139	forward 1	TM	Transmembrane
237	LI:018494.1:2001MAY17	140	145	forward 1	TM	Cytosolic
237	LI:018494.1:2001MAY17	146	168	forward 1	TM	Transmembrane
237	LI:018494.1:2001MAY17	169	187	forward 1	TM	Non-Cytosolic
237	LI:018494.1:2001MAY17	188	210	forward 1	TM	Transmembrane
237	LI:018494.1:2001MAY17	211	230	forward 1	TM	Cytosolic
237	LI:018494.1:2001MAY17	231	253	forward 1	TM	Transmembrane
237	LI:018494.1:2001MAY17	254	287	forward 1	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
237	U:018494.1:2001MAY17	288	310	forward 1	TM	Transmembrane
237	U:018494.1:2001MAY17	311	330	forward 1	TM	Cytosolic
237	U:018494.1:2001MAY17	331	353	forward 1	TM	Transmembrane
237	U:018494.1:2001MAY17	354	362	forward 1	TM	Non-Cytosolic
237	U:018494.1:2001MAY17	363	385	forward 1	TM	Transmembrane
237	U:018494.1:2001MAY17	386	391	forward 1	TM	Cytosolic
237	U:018494.1:2001MAY17	392	414	forward 1	TM	Transmembrane
237	U:018494.1:2001MAY17	415	469	forward 1	TM	Non-Cytosolic
237	U:018494.1:2001MAY17	470	492	forward 1	TM	Transmembrane
237	U:018494.1:2001MAY17	493	581	forward 1	TM	Cytosolic
237	U:018494.1:2001MAY17	582	604	forward 1	TM	Transmembrane
237	U:018494.1:2001MAY17	605	623	forward 1	TM	Non-Cytosolic
237	U:018494.1:2001MAY17	624	646	forward 1	TM	Transmembrane
237	U:018494.1:2001MAY17	647	765	forward 1	TM	Cytosolic
237	U:018494.1:2001MAY17	766	788	forward 1	TM	Transmembrane
237	U:018494.1:2001MAY17	789	791	forward 1	TM	Non-Cytosolic
237	U:018494.1:2001MAY17	792	814	forward 1	TM	Transmembrane
237	U:018494.1:2001MAY17	815	918	forward 1	TM	Cytosolic
237	U:018494.1:2001MAY17	1	459	forward 2	TM	Non-Cytosolic
237	U:018494.1:2001MAY17	460	482	forward 2	TM	Transmembrane
237	U:018494.1:2001MAY17	483	766	forward 2	TM	Cytosolic
237	U:018494.1:2001MAY17	767	789	forward 2	TM	Transmembrane
237	U:018494.1:2001MAY17	790	808	forward 2	TM	Non-Cytosolic
237	U:018494.1:2001MAY17	809	831	forward 2	TM	Transmembrane
237	U:018494.1:2001MAY17	832	918	forward 2	TM	Cytosolic
237	U:018494.1:2001MAY17	1	582	forward 3	TM	Non-Cytosolic
237	U:018494.1:2001MAY17	583	605	forward 3	TM	Transmembrane
237	U:018494.1:2001MAY17	606	611	forward 3	TM	Cytosolic
237	U:018494.1:2001MAY17	612	634	forward 3	TM	Transmembrane
237	U:018494.1:2001MAY17	635	661	forward 3	TM	Non-Cytosolic
237	U:018494.1:2001MAY17	662	684	forward 3	TM	Transmembrane
237	U:018494.1:2001MAY17	685	771	forward 3	TM	Cytosolic
237	U:018494.1:2001MAY17	772	794	forward 3	TM	Transmembrane
237	U:018494.1:2001MAY17	795	803	forward 3	TM	Non-Cytosolic
237	U:018494.1:2001MAY17	804	826	forward 3	TM	Transmembrane
237	U:018494.1:2001MAY17	827	917	forward 3	TM	Cytosolic
238	U:023518.2:2001MAY17	1	358	forward 1	TM	Non-Cytosolic
238	U:023518.2:2001MAY17	359	381	forward 1	TM	Transmembrane
238	U:023518.2:2001MAY17	382	410	forward 1	TM	Cytosolic
238	U:023518.2:2001MAY17	1	357	forward 2	TM	Non-Cytosolic
238	U:023518.2:2001MAY17	358	380	forward 2	TM	Transmembrane
238	U:023518.2:2001MAY17	381	410	forward 2	TM	Cytosolic
239	U:053488.46:2001MAY17	1	633	forward 2	TM	Non-Cytosolic
239	U:053488.46:2001MAY17	634	656	forward 2	TM	Transmembrane
239	U:053488.46:2001MAY17	657	676	forward 2	TM	Cytosolic
239	U:053488.46:2001MAY17	1	50	forward 3	TM	Cytosolic
239	U:053488.46:2001MAY17	51	73	forward 3	TM	Transmembrane
239	U:053488.46:2001MAY17	74	676	forward 3	TM	Non-Cytosolic
240	U:058298.27:2001MAY17	1	88	forward 2	TM	Cytosolic
240	U:058298.27:2001MAY17	89	111	forward 2	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
240	U:058298.27:2001MAY17	112	426	forward 2	TM	Non-Cytosolic
241	U:1110046.1:2001MAY17	1	544	forward 2	TM	Non-Cytosolic
241	U:1110046.1:2001MAY17	545	567	forward 2	TM	Transmembrane
241	U:1110046.1:2001MAY17	568	604	forward 2	TM	Cytosolic
241	U:1110046.1:2001MAY17	1	40	forward 3	TM	Cytosolic
241	U:1110046.1:2001MAY17	41	63	forward 3	TM	Transmembrane
241	U:1110046.1:2001MAY17	64	72	forward 3	TM	Non-Cytosolic
241	U:1110046.1:2001MAY17	73	95	forward 3	TM	Transmembrane
241	U:1110046.1:2001MAY17	96	115	forward 3	TM	Cytosolic
241	U:1110046.1:2001MAY17	116	138	forward 3	TM	Transmembrane
241	U:1110046.1:2001MAY17	139	171	forward 3	TM	Non-Cytosolic
241	U:1110046.1:2001MAY17	172	194	forward 3	TM	Transmembrane
241	U:1110046.1:2001MAY17	195	206	forward 3	TM	Cytosolic
241	U:1110046.1:2001MAY17	207	229	forward 3	TM	Transmembrane
241	U:1110046.1:2001MAY17	230	256	forward 3	TM	Non-Cytosolic
241	U:1110046.1:2001MAY17	257	276	forward 3	TM	Transmembrane
241	U:1110046.1:2001MAY17	277	399	forward 3	TM	Cytosolic
241	U:1110046.1:2001MAY17	400	422	forward 3	TM	Transmembrane
241	U:1110046.1:2001MAY17	423	472	forward 3	TM	Non-Cytosolic
241	U:1110046.1:2001MAY17	473	495	forward 3	TM	Transmembrane
241	U:1110046.1:2001MAY17	496	541	forward 3	TM	Cytosolic
241	U:1110046.1:2001MAY17	542	561	forward 3	TM	Transmembrane
241	U:1110046.1:2001MAY17	562	575	forward 3	TM	Non-Cytosolic
241	U:1110046.1:2001MAY17	576	593	forward 3	TM	Transmembrane
241	U:1110046.1:2001MAY17	594	604	forward 3	TM	Cytosolic
242	U:1166752.11:2001MAY17	1	507	forward 3	TM	Non-Cytosolic
242	U:1166752.11:2001MAY17	508	530	forward 3	TM	Transmembrane
242	U:1166752.11:2001MAY17	531	588	forward 3	TM	Cytosolic
243	U:1173766.1:2001MAY17	1	778	forward 2	TM	Non-Cytosolic
243	U:1173766.1:2001MAY17	779	801	forward 2	TM	Transmembrane
243	U:1173766.1:2001MAY17	802	821	forward 2	TM	Cytosolic
243	U:1173766.1:2001MAY17	822	839	forward 2	TM	Transmembrane
243	U:1173766.1:2001MAY17	840	879	forward 2	TM	Non-Cytosolic
243	U:1173766.1:2001MAY17	880	899	forward 2	TM	Transmembrane
243	U:1173766.1:2001MAY17	900	1030	forward 2	TM	Cytosolic
244	U:1177952.4:2001MAY17	1	248	forward 1	TM	Non-Cytosolic
244	U:1177952.4:2001MAY17	249	271	forward 1	TM	Transmembrane
244	U:1177952.4:2001MAY17	272	338	forward 1	TM	Cytosolic
244	U:1177952.4:2001MAY17	339	361	forward 1	TM	Transmembrane
244	U:1177952.4:2001MAY17	362	754	forward 1	TM	Non-Cytosolic
245	U:1178064.3:2001MAY17	1	1139	forward 3	TM	Non-Cytosolic
245	U:1178064.3:2001MAY17	1140	1162	forward 3	TM	Transmembrane
245	U:1178064.3:2001MAY17	1163	1536	forward 3	TM	Cytosolic
246	U:1183121.1:2001MAY17	1	437	forward 1	TM	Non-Cytosolic
246	U:1183121.1:2001MAY17	438	460	forward 1	TM	Transmembrane
246	U:1183121.1:2001MAY17	461	511	forward 1	TM	Cytosolic
246	U:1183121.1:2001MAY17	512	534	forward 1	TM	Transmembrane
246	U:1183121.1:2001MAY17	535	590	forward 1	TM	Non-Cytosolic
246	U:1183121.1:2001MAY17	591	613	forward 1	TM	Transmembrane
246	U:1183121.1:2001MAY17	614	868	forward 1	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
246	U:1183121.1:2001MAY17	869	891	forward 1	TM	Transmembrane
246	U:1183121.1:2001MAY17	892	913	forward 1	TM	Non-Cytosolic
246	U:1183121.1:2001MAY17	914	936	forward 1	TM	Transmembrane
246	U:1183121.1:2001MAY17	937	948	forward 1	TM	Cytosolic
246	U:1183121.1:2001MAY17	949	971	forward 1	TM	Transmembrane
246	U:1183121.1:2001MAY17	972	1011	forward 1	TM	Non-Cytosolic
246	U:1183121.1:2001MAY17	1012	1034	forward 1	TM	Transmembrane
246	U:1183121.1:2001MAY17	1035	1057	forward 1	TM	Cytosolic
246	U:1183121.1:2001MAY17	1	913	forward 2	TM	Non-Cytosolic
246	U:1183121.1:2001MAY17	914	936	forward 2	TM	Transmembrane
246	U:1183121.1:2001MAY17	937	948	forward 2	TM	Cytosolic
246	U:1183121.1:2001MAY17	949	971	forward 2	TM	Transmembrane
246	U:1183121.1:2001MAY17	972	1009	forward 2	TM	Non-Cytosolic
246	U:1183121.1:2001MAY17	1010	1032	forward 2	TM	Transmembrane
246	U:1183121.1:2001MAY17	1033	1057	forward 2	TM	Cytosolic
246	U:1183121.1:2001MAY17	1	573	forward 3	TM	Non-Cytosolic
246	U:1183121.1:2001MAY17	574	596	forward 3	TM	Transmembrane
246	U:1183121.1:2001MAY17	597	791	forward 3	TM	Cytosolic
246	U:1183121.1:2001MAY17	792	809	forward 3	TM	Transmembrane
246	U:1183121.1:2001MAY17	810	873	forward 3	TM	Non-Cytosolic
246	U:1183121.1:2001MAY17	874	896	forward 3	TM	Transmembrane
246	U:1183121.1:2001MAY17	897	915	forward 3	TM	Cytosolic
246	U:1183121.1:2001MAY17	916	938	forward 3	TM	Transmembrane
246	U:1183121.1:2001MAY17	939	952	forward 3	TM	Non-Cytosolic
246	U:1183121.1:2001MAY17	953	975	forward 3	TM	Transmembrane
246	U:1183121.1:2001MAY17	976	1056	forward 3	TM	Cytosolic
247	U:1190431.13:2001MAY17	1	1983	forward 1	TM	Non-Cytosolic
247	U:1190431.13:2001MAY17	1984	2006	forward 1	TM	Transmembrane
247	U:1190431.13:2001MAY17	2007	2155	forward 1	TM	Cytosolic
247	U:1190431.13:2001MAY17	2156	2175	forward 1	TM	Transmembrane
247	U:1190431.13:2001MAY17	2176	2194	forward 1	TM	Non-Cytosolic
247	U:1190431.13:2001MAY17	2195	2217	forward 1	TM	Transmembrane
247	U:1190431.13:2001MAY17	2218	2287	forward 1	TM	Cytosolic
247	U:1190431.13:2001MAY17	2288	2307	forward 1	TM	Transmembrane
247	U:1190431.13:2001MAY17	2308	2461	forward 1	TM	Non-Cytosolic
247	U:1190431.13:2001MAY17	1	1381	forward 2	TM	Non-Cytosolic
247	U:1190431.13:2001MAY17	1382	1404	forward 2	TM	Transmembrane
247	U:1190431.13:2001MAY17	1405	1584	forward 2	TM	Cytosolic
247	U:1190431.13:2001MAY17	1585	1603	forward 2	TM	Transmembrane
247	U:1190431.13:2001MAY17	1604	2209	forward 2	TM	Non-Cytosolic
247	U:1190431.13:2001MAY17	2210	2232	forward 2	TM	Transmembrane
247	U:1190431.13:2001MAY17	2233	2236	forward 2	TM	Cytosolic
247	U:1190431.13:2001MAY17	2237	2254	forward 2	TM	Transmembrane
247	U:1190431.13:2001MAY17	2255	2461	forward 2	TM	Non-Cytosolic
247	U:1190431.13:2001MAY17	1	2209	forward 3	TM	Non-Cytosolic
247	U:1190431.13:2001MAY17	2210	2232	forward 3	TM	Transmembrane
247	U:1190431.13:2001MAY17	2233	2461	forward 3	TM	Cytosolic
248	U:199121.14:2001MAY17	1	831	forward 1	TM	Non-Cytosolic
248	U:199121.14:2001MAY17	832	854	forward 1	TM	Transmembrane
248	U:199121.14:2001MAY17	855	860	forward 1	TM	Cytosolic



TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
248	U:199121.14:2001MAY17	861	880	forward 1	TM	Transmembrane
248	U:199121.14:2001MAY17	881	1248	forward 1	TM	Non-Cytosolic
248	U:199121.14:2001MAY17	1249	1268	forward 1	TM	Transmembrane
248	U:199121.14:2001MAY17	1269	1286	forward 1	TM	Cytosolic
248	U:199121.14:2001MAY17	1	1158	forward 2	TM	Non-Cytosolic
248	U:199121.14:2001MAY17	1159	1181	forward 2	TM	Transmembrane
248	U:199121.14:2001MAY17	1182	1201	forward 2	TM	Cytosolic
248	U:199121.14:2001MAY17	1202	1224	forward 2	TM	Transmembrane
248	U:199121.14:2001MAY17	1225	1243	forward 2	TM	Non-Cytosolic
248	U:199121.14:2001MAY17	1244	1266	forward 2	TM	Transmembrane
248	U:199121.14:2001MAY17	1267	1286	forward 2	TM	Cytosolic
248	U:199121.14:2001MAY17	1	725	forward 3	TM	Non-Cytosolic
248	U:199121.14:2001MAY17	726	745	forward 3	TM	Transmembrane
248	U:199121.14:2001MAY17	746	952	forward 3	TM	Cytosolic
248	U:199121.14:2001MAY17	953	975	forward 3	TM	Transmembrane
248	U:199121.14:2001MAY17	976	998	forward 3	TM	Non-Cytosolic
248	U:199121.14:2001MAY17	999	1021	forward 3	TM	Transmembrane
248	U:199121.14:2001MAY17	1022	1051	forward 3	TM	Cytosolic
248	U:199121.14:2001MAY17	1052	1074	forward 3	TM	Transmembrane
248	U:199121.14:2001MAY17	1075	1162	forward 3	TM	Non-Cytosolic
248	U:199121.14:2001MAY17	1163	1181	forward 3	TM	Transmembrane
248	U:199121.14:2001MAY17	1182	1201	forward 3	TM	Cytosolic
248	U:199121.14:2001MAY17	1202	1224	forward 3	TM	Transmembrane
248	U:199121.14:2001MAY17	1225	1243	forward 3	TM	Non-Cytosolic
248	U:199121.14:2001MAY17	1244	1266	forward 3	TM	Transmembrane
248	U:199121.14:2001MAY17	1267	1286	forward 3	TM	Cytosolic
249	U:202630.5:2001MAY17	1	326	forward 2	TM	Non-Cytosolic
249	U:202630.5:2001MAY17	327	349	forward 2	TM	Transmembrane
249	U:202630.5:2001MAY17	350	355	forward 2	TM	Cytosolic
249	U:202630.5:2001MAY17	356	378	forward 2	TM	Transmembrane
249	U:202630.5:2001MAY17	379	397	forward 2	TM	Non-Cytosolic
249	U:202630.5:2001MAY17	398	420	forward 2	TM	Transmembrane
249	U:202630.5:2001MAY17	421	440	forward 2	TM	Cytosolic
249	U:202630.5:2001MAY17	441	463	forward 2	TM	Transmembrane
249	U:202630.5:2001MAY17	464	485	forward 2	TM	Non-Cytosolic
249	U:202630.5:2001MAY17	486	508	forward 2	TM	Transmembrane
249	U:202630.5:2001MAY17	509	528	forward 2	TM	Cytosolic
249	U:202630.5:2001MAY17	529	551	forward 2	TM	Transmembrane
249	U:202630.5:2001MAY17	552	740	forward 2	TM	Non-Cytosolic
250	U:2034488.1:2001MAY17	1	386	forward 2	TM	Non-Cytosolic
250	U:2034488.1:2001MAY17	387	409	forward 2	TM	Transmembrane
250	U:2034488.1:2001MAY17	410	424	forward 2	TM	Cytosolic
251	U:2051434.8:2001MAY17	1	607	forward 1	TM	Non-Cytosolic
251	U:2051434.8:2001MAY17	608	630	forward 1	TM	Transmembrane
251	U:2051434.8:2001MAY17	631	652	forward 1	TM	Cytosolic
251	U:2051434.8:2001MAY17	653	675	forward 1	TM	Transmembrane
251	U:2051434.8:2001MAY17	676	698	forward 1	TM	Non-Cytosolic
251	U:2051434.8:2001MAY17	1	553	forward 3	TM	Non-Cytosolic
251	U:2051434.8:2001MAY17	554	576	forward 3	TM	Transmembrane
251	U:2051434.8:2001MAY17	577	651	forward 3	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
251	U:2051434.8:2001MAY17	652	674	forward 3	TM	Transmembrane
251	U:2051434.8:2001MAY17	675	697	forward 3	TM	Non-Cytosolic
252	U:2118475.9:2001MAY17	1	432	forward 1	TM	Non-Cytosolic
252	U:2118475.9:2001MAY17	433	455	forward 1	TM	Transmembrane
252	U:2118475.9:2001MAY17	456	456	forward 1	TM	Cytosolic
252	U:2118475.9:2001MAY17	1	431	forward 3	TM	Non-Cytosolic
252	U:2118475.9:2001MAY17	432	454	forward 3	TM	Transmembrane
252	U:2118475.9:2001MAY17	455	456	forward 3	TM	Cytosolic
253	U:218849.24:2001MAY17	1	1133	forward 1	TM	Non-Cytosolic
253	U:218849.24:2001MAY17	1134	1156	forward 1	TM	Transmembrane
253	U:218849.24:2001MAY17	1157	1167	forward 1	TM	Cytosolic
253	U:218849.24:2001MAY17	1168	1190	forward 1	TM	Transmembrane
253	U:218849.24:2001MAY17	1191	1193	forward 1	TM	Non-Cytosolic
253	U:218849.24:2001MAY17	1194	1213	forward 1	TM	Transmembrane
253	U:218849.24:2001MAY17	1214	1293	forward 1	TM	Cytosolic
253	U:218849.24:2001MAY17	1294	1316	forward 1	TM	Transmembrane
253	U:218849.24:2001MAY17	1317	1350	forward 1	TM	Non-Cytosolic
253	U:218849.24:2001MAY17	1351	1373	forward 1	TM	Transmembrane
253	U:218849.24:2001MAY17	1374	1385	forward 1	TM	Cytosolic
253	U:218849.24:2001MAY17	1386	1408	forward 1	TM	Transmembrane
253	U:218849.24:2001MAY17	1409	1493	forward 1	TM	Non-Cytosolic
253	U:218849.24:2001MAY17	1	211	forward 2	TM	Cytosolic
253	U:218849.24:2001MAY17	212	234	forward 2	TM	Transmembrane
253	U:218849.24:2001MAY17	235	286	forward 2	TM	Non-Cytosolic
253	U:218849.24:2001MAY17	287	309	forward 2	TM	Transmembrane
253	U:218849.24:2001MAY17	310	321	forward 2	TM	Cytosolic
253	U:218849.24:2001MAY17	322	344	forward 2	TM	Transmembrane
253	U:218849.24:2001MAY17	345	369	forward 2	TM	Non-Cytosolic
253	U:218849.24:2001MAY17	370	392	forward 2	TM	Transmembrane
253	U:218849.24:2001MAY17	393	466	forward 2	TM	Cytosolic
253	U:218849.24:2001MAY17	467	489	forward 2	TM	Transmembrane
253	U:218849.24:2001MAY17	490	503	forward 2	TM	Non-Cytosolic
253	U:218849.24:2001MAY17	504	526	forward 2	TM	Transmembrane
253	U:218849.24:2001MAY17	527	537	forward 2	TM	Cytosolic
253	U:218849.24:2001MAY17	538	560	forward 2	TM	Transmembrane
253	U:218849.24:2001MAY17	561	658	forward 2	TM	Non-Cytosolic
253	U:218849.24:2001MAY17	659	681	forward 2	TM	Transmembrane
253	U:218849.24:2001MAY17	682	745	forward 2	TM	Cytosolic
253	U:218849.24:2001MAY17	746	768	forward 2	TM	Transmembrane
253	U:218849.24:2001MAY17	769	1190	forward 2	TM	Non-Cytosolic
253	U:218849.24:2001MAY17	1191	1213	forward 2	TM	Transmembrane
253	U:218849.24:2001MAY17	1214	1291	forward 2	TM	Cytosolic
253	U:218849.24:2001MAY17	1292	1314	forward 2	TM	Transmembrane
253	U:218849.24:2001MAY17	1315	1350	forward 2	TM	Non-Cytosolic
253	U:218849.24:2001MAY17	1351	1373	forward 2	TM	Transmembrane
253	U:218849.24:2001MAY17	1374	1392	forward 2	TM	Cytosolic
253	U:218849.24:2001MAY17	1393	1415	forward 2	TM	Transmembrane
253	U:218849.24:2001MAY17	1416	1493	forward 2	TM	Non-Cytosolic
253	U:218849.24:2001MAY17	1	1404	forward 3	TM	Non-Cytosolic
253	U:218849.24:2001MAY17	1405	1427	forward 3	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
253	U:218849.24:2001MAY17	1428	1492	forward 3	TM	Cytosolic
254	U:2199824.5:2001MAY17	1	27	forward 2	TM	Cytosolic
254	U:2199824.5:2001MAY17	28	45	forward 2	TM	Transmembrane
254	U:2199824.5:2001MAY17	46	623	forward 2	TM	Non-Cytosolic
254	U:2199824.5:2001MAY17	1	594	forward 3	TM	Non-Cytosolic
254	U:2199824.5:2001MAY17	595	617	forward 3	TM	Transmembrane
254	U:2199824.5:2001MAY17	618	623	forward 3	TM	Cytosolic
255	U:233018.32:2001MAY17	1	872	forward 1	TM	Non-Cytosolic
255	U:233018.32:2001MAY17	873	895	forward 1	TM	Transmembrane
255	U:233018.32:2001MAY17	896	907	forward 1	TM	Cytosolic
255	U:233018.32:2001MAY17	908	927	forward 1	TM	Transmembrane
255	U:233018.32:2001MAY17	928	1420	forward 1	TM	Non-Cytosolic
255	U:233018.32:2001MAY17	1	784	forward 2	TM	Non-Cytosolic
255	U:233018.32:2001MAY17	785	807	forward 2	TM	Transmembrane
255	U:233018.32:2001MAY17	808	854	forward 2	TM	Cytosolic
255	U:233018.32:2001MAY17	855	877	forward 2	TM	Transmembrane
255	U:233018.32:2001MAY17	878	891	forward 2	TM	Non-Cytosolic
255	U:233018.32:2001MAY17	892	914	forward 2	TM	Transmembrane
255	U:233018.32:2001MAY17	915	1033	forward 2	TM	Cytosolic
255	U:233018.32:2001MAY17	1034	1056	forward 2	TM	Transmembrane
255	U:233018.32:2001MAY17	1057	1420	forward 2	TM	Non-Cytosolic
255	U:233018.32:2001MAY17	1	545	forward 3	TM	Non-Cytosolic
255	U:233018.32:2001MAY17	546	568	forward 3	TM	Transmembrane
255	U:233018.32:2001MAY17	569	606	forward 3	TM	Cytosolic
255	U:233018.32:2001MAY17	607	629	forward 3	TM	Transmembrane
255	U:233018.32:2001MAY17	630	1420	forward 3	TM	Non-Cytosolic
256	U:236295.8:2001MAY17	1	91	forward 3	TM	Cytosolic
256	U:236295.8:2001MAY17	92	114	forward 3	TM	Transmembrane
256	U:236295.8:2001MAY17	115	183	forward 3	TM	Non-Cytosolic
256	U:236295.8:2001MAY17	184	202	forward 3	TM	Transmembrane
256	U:236295.8:2001MAY17	203	429	forward 3	TM	Cytosolic
257	U:286989.14:2001MAY17	1	677	forward 1	TM	Non-Cytosolic
257	U:286989.14:2001MAY17	678	700	forward 1	TM	Transmembrane
257	U:286989.14:2001MAY17	701	706	forward 1	TM	Cytosolic
257	U:286989.14:2001MAY17	707	729	forward 1	TM	Transmembrane
257	U:286989.14:2001MAY17	730	776	forward 1	TM	Non-Cytosolic
257	U:286989.14:2001MAY17	777	799	forward 1	TM	Transmembrane
257	U:286989.14:2001MAY17	800	969	forward 1	TM	Cytosolic
257	U:286989.14:2001MAY17	970	992	forward 1	TM	Transmembrane
257	U:286989.14:2001MAY17	993	1006	forward 1	TM	Non-Cytosolic
257	U:286989.14:2001MAY17	1007	1029	forward 1	TM	Transmembrane
257	U:286989.14:2001MAY17	1030	1048	forward 1	TM	Cytosolic
257	U:286989.14:2001MAY17	1049	1071	forward 1	TM	Transmembrane
257	U:286989.14:2001MAY17	1072	1085	forward 1	TM	Non-Cytosolic
257	U:286989.14:2001MAY17	1086	1105	forward 1	TM	Transmembrane
257	U:286989.14:2001MAY17	1106	1116	forward 1	TM	Cytosolic
257	U:286989.14:2001MAY17	1117	1139	forward 1	TM	Transmembrane
257	U:286989.14:2001MAY17	1140	1203	forward 1	TM	Non-Cytosolic
257	U:286989.14:2001MAY17	1	348	forward 2	TM	Non-Cytosolic
257	U:286989.14:2001MAY17	349	371	forward 2	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
257	U:286989.14:2001MAY17	372	664	forward 2	TM	Cytosolic
257	U:286989.14:2001MAY17	665	687	forward 2	TM	Transmembrane
257	U:286989.14:2001MAY17	688	706	forward 2	TM	Non-Cytosolic
257	U:286989.14:2001MAY17	707	729	forward 2	TM	Transmembrane
257	U:286989.14:2001MAY17	730	777	forward 2	TM	Cytosolic
257	U:286989.14:2001MAY17	778	800	forward 2	TM	Transmembrane
257	U:286989.14:2001MAY17	801	854	forward 2	TM	Non-Cytosolic
257	U:286989.14:2001MAY17	855	877	forward 2	TM	Transmembrane
257	U:286989.14:2001MAY17	878	1001	forward 2	TM	Cytosolic
257	U:286989.14:2001MAY17	1002	1024	forward 2	TM	Transmembrane
257	U:286989.14:2001MAY17	1025	1086	forward 2	TM	Non-Cytosolic
257	U:286989.14:2001MAY17	1087	1109	forward 2	TM	Transmembrane
257	U:286989.14:2001MAY17	1110	1115	forward 2	TM	Cytosolic
257	U:286989.14:2001MAY17	1116	1138	forward 2	TM	Transmembrane
257	U:286989.14:2001MAY17	1139	1141	forward 2	TM	Non-Cytosolic
257	U:286989.14:2001MAY17	1142	1164	forward 2	TM	Transmembrane
257	U:286989.14:2001MAY17	1165	1202	forward 2	TM	Cytosolic
257	U:286989.14:2001MAY17	1	656	forward 3	TM	Non-Cytosolic
257	U:286989.14:2001MAY17	657	688	forward 3	TM	Transmembrane
257	U:286989.14:2001MAY17	689	707	forward 3	TM	Cytosolic
257	U:286989.14:2001MAY17	708	729	forward 3	TM	Transmembrane
257	U:286989.14:2001MAY17	730	778	forward 3	TM	Non-Cytosolic
257	U:286989.14:2001MAY17	779	798	forward 3	TM	Transmembrane
257	U:286989.14:2001MAY17	799	827	forward 3	TM	Cytosolic
257	U:286989.14:2001MAY17	828	850	forward 3	TM	Transmembrane
257	U:286989.14:2001MAY17	851	882	forward 3	TM	Non-Cytosolic
257	U:286989.14:2001MAY17	883	905	forward 3	TM	Transmembrane
257	U:286989.14:2001MAY17	906	966	forward 3	TM	Cytosolic
257	U:286989.14:2001MAY17	967	989	forward 3	TM	Transmembrane
257	U:286989.14:2001MAY17	990	1074	forward 3	TM	Non-Cytosolic
257	U:286989.14:2001MAY17	1075	1097	forward 3	TM	Transmembrane
257	U:286989.14:2001MAY17	1098	1101	forward 3	TM	Cytosolic
257	U:286989.14:2001MAY17	1102	1119	forward 3	TM	Transmembrane
257	U:286989.14:2001MAY17	1120	1123	forward 3	TM	Non-Cytosolic
257	U:286989.14:2001MAY17	1124	1146	forward 3	TM	Transmembrane
257	U:286989.14:2001MAY17	1147	1202	forward 3	TM	Cytosolic
258	U:345320.4:2001MAY17	1	1488	forward 1	TM	Non-Cytosolic
258	U:345320.4:2001MAY17	1489	1511	forward 1	TM	Transmembrane
258	U:345320.4:2001MAY17	1512	1517	forward 1	TM	Cytosolic
258	U:345320.4:2001MAY17	1518	1540	forward 1	TM	Transmembrane
258	U:345320.4:2001MAY17	1541	1660	forward 1	TM	Non-Cytosolic
258	U:345320.4:2001MAY17	1661	1683	forward 1	TM	Transmembrane
258	U:345320.4:2001MAY17	1684	1776	forward 1	TM	Cytosolic
258	U:345320.4:2001MAY17	1777	1799	forward 1	TM	Transmembrane
258	U:345320.4:2001MAY17	1800	2093	forward 1	TM	Non-Cytosolic
258	U:345320.4:2001MAY17	1	6	forward 2	TM	Cytosolic
258	U:345320.4:2001MAY17	7	29	forward 2	TM	Transmembrane
258	U:345320.4:2001MAY17	30	642	forward 2	TM	Non-Cytosolic
258	U:345320.4:2001MAY17	643	665	forward 2	TM	Transmembrane
258	U:345320.4:2001MAY17	666	1168	forward 2	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
258	U:345320.4:2001MAY17	1169	1191	forward 2	TM	Transmembrane
258	U:345320.4:2001MAY17	1192	1274	forward 2	TM	Non-Cytosolic
258	U:345320.4:2001MAY17	1275	1297	forward 2	TM	Transmembrane
258	U:345320.4:2001MAY17	1298	1431	forward 2	TM	Cytosolic
258	U:345320.4:2001MAY17	1432	1454	forward 2	TM	Transmembrane
258	U:345320.4:2001MAY17	1455	1501	forward 2	TM	Non-Cytosolic
258	U:345320.4:2001MAY17	1502	1524	forward 2	TM	Transmembrane
258	U:345320.4:2001MAY17	1525	1649	forward 2	TM	Cytosolic
258	U:345320.4:2001MAY17	1650	1672	forward 2	TM	Transmembrane
258	U:345320.4:2001MAY17	1673	1707	forward 2	TM	Non-Cytosolic
258	U:345320.4:2001MAY17	1708	1730	forward 2	TM	Transmembrane
258	U:345320.4:2001MAY17	1731	1767	forward 2	TM	Cytosolic
258	U:345320.4:2001MAY17	1768	1790	forward 2	TM	Transmembrane
258	U:345320.4:2001MAY17	1791	2093	forward 2	TM	Non-Cytosolic
258	U:345320.4:2001MAY17	1	6	forward 3	TM	Cytosolic
258	U:345320.4:2001MAY17	7	24	forward 3	TM	Transmembrane
258	U:345320.4:2001MAY17	25	1409	forward 3	TM	Non-Cytosolic
258	U:345320.4:2001MAY17	1410	1432	forward 3	TM	Transmembrane
258	U:345320.4:2001MAY17	1433	1436	forward 3	TM	Cytosolic
258	U:345320.4:2001MAY17	1437	1459	forward 3	TM	Transmembrane
258	U:345320.4:2001MAY17	1460	1659	forward 3	TM	Non-Cytosolic
258	U:345320.4:2001MAY17	1660	1682	forward 3	TM	Transmembrane
258	U:345320.4:2001MAY17	1683	1752	forward 3	TM	Cytosolic
258	U:345320.4:2001MAY17	1753	1775	forward 3	TM	Transmembrane
258	U:345320.4:2001MAY17	1776	2092	forward 3	TM	Non-Cytosolic
259	U:355693.18:2001MAY17	1	1472	forward 1	TM	Non-Cytosolic
259	U:355693.18:2001MAY17	1473	1495	forward 1	TM	Transmembrane
259	U:355693.18:2001MAY17	1496	2222	forward 1	TM	Cytosolic
259	U:355693.18:2001MAY17	2223	2245	forward 1	TM	Transmembrane
259	U:355693.18:2001MAY17	2246	2273	forward 1	TM	Non-Cytosolic
259	U:355693.18:2001MAY17	2274	2296	forward 1	TM	Transmembrane
259	U:355693.18:2001MAY17	2297	2378	forward 1	TM	Cytosolic
259	U:355693.18:2001MAY17	1	2273	forward 3	TM	Non-Cytosolic
259	U:355693.18:2001MAY17	2274	2296	forward 3	TM	Transmembrane
259	U:355693.18:2001MAY17	2297	2378	forward 3	TM	Cytosolic
260	U:359876.1:2001MAY17	1	585	forward 1	TM	Non-Cytosolic
260	U:359876.1:2001MAY17	586	605	forward 1	TM	Transmembrane
260	U:359876.1:2001MAY17	606	630	forward 1	TM	Cytosolic
260	U:359876.1:2001MAY17	631	653	forward 1	TM	Transmembrane
260	U:359876.1:2001MAY17	654	657	forward 1	TM	Non-Cytosolic
260	U:359876.1:2001MAY17	658	677	forward 1	TM	Transmembrane
260	U:359876.1:2001MAY17	678	741	forward 1	TM	Cytosolic
260	U:359876.1:2001MAY17	742	764	forward 1	TM	Transmembrane
260	U:359876.1:2001MAY17	765	913	forward 1	TM	Non-Cytosolic
260	U:359876.1:2001MAY17	1	191	forward 2	TM	Non-Cytosolic
260	U:359876.1:2001MAY17	192	214	forward 2	TM	Transmembrane
260	U:359876.1:2001MAY17	215	225	forward 2	TM	Cytosolic
260	U:359876.1:2001MAY17	226	248	forward 2	TM	Transmembrane
260	U:359876.1:2001MAY17	249	262	forward 2	TM	Non-Cytosolic
260	U:359876.1:2001MAY17	263	285	forward 2	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
260	U:359876.1:2001MAY17	286	305	forward 2	TM	Cytosolic
260	U:359876.1:2001MAY17	306	328	forward 2	TM	Transmembrane
260	U:359876.1:2001MAY17	329	361	forward 2	TM	Non-Cytosolic
260	U:359876.1:2001MAY17	362	384	forward 2	TM	Transmembrane
260	U:359876.1:2001MAY17	385	404	forward 2	TM	Cytosolic
260	U:359876.1:2001MAY17	405	427	forward 2	TM	Transmembrane
260	U:359876.1:2001MAY17	428	436	forward 2	TM	Non-Cytosolic
260	U:359876.1:2001MAY17	437	456	forward 2	TM	Transmembrane
260	U:359876.1:2001MAY17	457	534	forward 2	TM	Cytosolic
260	U:359876.1:2001MAY17	535	557	forward 2	TM	Transmembrane
260	U:359876.1:2001MAY17	558	585	forward 2	TM	Non-Cytosolic
260	U:359876.1:2001MAY17	586	605	forward 2	TM	Transmembrane
260	U:359876.1:2001MAY17	606	617	forward 2	TM	Cytosolic
260	U:359876.1:2001MAY17	618	637	forward 2	TM	Transmembrane
260	U:359876.1:2001MAY17	638	656	forward 2	TM	Non-Cytosolic
260	U:359876.1:2001MAY17	657	679	forward 2	TM	Transmembrane
260	U:359876.1:2001MAY17	680	739	forward 2	TM	Cytosolic
260	U:359876.1:2001MAY17	740	762	forward 2	TM	Transmembrane
260	U:359876.1:2001MAY17	763	912	forward 2	TM	Non-Cytosolic
260	U:359876.1:2001MAY17	1	368	forward 3	TM	Non-Cytosolic
260	U:359876.1:2001MAY17	369	391	forward 3	TM	Transmembrane
260	U:359876.1:2001MAY17	392	616	forward 3	TM	Cytosolic
260	U:359876.1:2001MAY17	617	639	forward 3	TM	Transmembrane
260	U:359876.1:2001MAY17	640	648	forward 3	TM	Non-Cytosolic
260	U:359876.1:2001MAY17	649	671	forward 3	TM	Transmembrane
260	U:359876.1:2001MAY17	672	705	forward 3	TM	Cytosolic
260	U:359876.1:2001MAY17	706	725	forward 3	TM	Transmembrane
260	U:359876.1:2001MAY17	726	734	forward 3	TM	Non-Cytosolic
260	U:359876.1:2001MAY17	735	757	forward 3	TM	Transmembrane
260	U:359876.1:2001MAY17	758	835	forward 3	TM	Cytosolic
260	U:359876.1:2001MAY17	836	855	forward 3	TM	Transmembrane
260	U:359876.1:2001MAY17	856	869	forward 3	TM	Non-Cytosolic
260	U:359876.1:2001MAY17	870	892	forward 3	TM	Transmembrane
260	U:359876.1:2001MAY17	893	912	forward 3	TM	Cytosolic
261	U:406664.32:2001MAY17	1	705	forward 1	TM	Non-Cytosolic
261	U:406664.32:2001MAY17	706	728	forward 1	TM	Transmembrane
261	U:406664.32:2001MAY17	729	951	forward 1	TM	Cytosolic
261	U:406664.32:2001MAY17	952	974	forward 1	TM	Transmembrane
261	U:406664.32:2001MAY17	975	977	forward 1	TM	Non-Cytosolic
261	U:406664.32:2001MAY17	978	997	forward 1	TM	Transmembrane
261	U:406664.32:2001MAY17	998	1017	forward 1	TM	Cytosolic
261	U:406664.32:2001MAY17	1018	1040	forward 1	TM	Transmembrane
261	U:406664.32:2001MAY17	1041	1076	forward 1	TM	Non-Cytosolic
261	U:406664.32:2001MAY17	1077	1099	forward 1	TM	Transmembrane
261	U:406664.32:2001MAY17	1100	1166	forward 1	TM	Cytosolic
261	U:406664.32:2001MAY17	1	951	forward 2	TM	Non-Cytosolic
261	U:406664.32:2001MAY17	952	974	forward 2	TM	Transmembrane
261	U:406664.32:2001MAY17	975	1071	forward 2	TM	Cytosolic
261	U:406664.32:2001MAY17	1072	1094	forward 2	TM	Transmembrane
261	U:406664.32:2001MAY17	1095	1113	forward 2	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
261	U:406664.32:2001MAY17	1114	1136	forward 2	TM	Transmembrane
261	U:406664.32:2001MAY17	1137	1166	forward 2	TM	Cytosolic
261	U:406664.32:2001MAY17	1	704	forward 3	TM	Non-Cytosolic
261	U:406664.32:2001MAY17	705	727	forward 3	TM	Transmembrane
261	U:406664.32:2001MAY17	728	910	forward 3	TM	Cytosolic
261	U:406664.32:2001MAY17	911	930	forward 3	TM	Transmembrane
261	U:406664.32:2001MAY17	931	1027	forward 3	TM	Non-Cytosolic
261	U:406664.32:2001MAY17	1028	1050	forward 3	TM	Transmembrane
261	U:406664.32:2001MAY17	1051	1069	forward 3	TM	Cytosolic
261	U:406664.32:2001MAY17	1070	1092	forward 3	TM	Transmembrane
261	U:406664.32:2001MAY17	1093	1111	forward 3	TM	Non-Cytosolic
261	U:406664.32:2001MAY17	1112	1134	forward 3	TM	Transmembrane
261	U:406664.32:2001MAY17	1135	1166	forward 3	TM	Cytosolic
262	U:410324.1:2001MAY17	1	1308	forward 1	TM	Non-Cytosolic
262	U:410324.1:2001MAY17	1309	1331	forward 1	TM	Transmembrane
262	U:410324.1:2001MAY17	1332	1351	forward 1	TM	Cytosolic
262	U:410324.1:2001MAY17	1352	1374	forward 1	TM	Transmembrane
262	U:410324.1:2001MAY17	1375	1419	forward 1	TM	Non-Cytosolic
262	U:410324.1:2001MAY17	1	59	forward 2	TM	Cytosolic
262	U:410324.1:2001MAY17	60	82	forward 2	TM	Transmembrane
262	U:410324.1:2001MAY17	83	1006	forward 2	TM	Non-Cytosolic
262	U:410324.1:2001MAY17	1007	1029	forward 2	TM	Transmembrane
262	U:410324.1:2001MAY17	1030	1194	forward 2	TM	Cytosolic
262	U:410324.1:2001MAY17	1195	1217	forward 2	TM	Transmembrane
262	U:410324.1:2001MAY17	1218	1236	forward 2	TM	Non-Cytosolic
262	U:410324.1:2001MAY17	1237	1259	forward 2	TM	Transmembrane
262	U:410324.1:2001MAY17	1260	1335	forward 2	TM	Cytosolic
262	U:410324.1:2001MAY17	1336	1358	forward 2	TM	Transmembrane
262	U:410324.1:2001MAY17	1359	1419	forward 2	TM	Non-Cytosolic
262	U:410324.1:2001MAY17	1	62	forward 3	TM	Cytosolic
262	U:410324.1:2001MAY17	63	85	forward 3	TM	Transmembrane
262	U:410324.1:2001MAY17	86	1194	forward 3	TM	Non-Cytosolic
262	U:410324.1:2001MAY17	1195	1217	forward 3	TM	Transmembrane
262	U:410324.1:2001MAY17	1218	1335	forward 3	TM	Cytosolic
262	U:410324.1:2001MAY17	1336	1358	forward 3	TM	Transmembrane
262	U:410324.1:2001MAY17	1359	1361	forward 3	TM	Non-Cytosolic
262	U:410324.1:2001MAY17	1362	1384	forward 3	TM	Transmembrane
262	U:410324.1:2001MAY17	1385	1418	forward 3	TM	Cytosolic
263	U:414376.12:2001MAY17	1	464	forward 2	TM	Non-Cytosolic
263	U:414376.12:2001MAY17	465	487	forward 2	TM	Transmembrane
263	U:414376.12:2001MAY17	488	542	forward 2	TM	Cytosolic
263	U:414376.12:2001MAY17	543	565	forward 2	TM	Transmembrane
263	U:414376.12:2001MAY17	566	579	forward 2	TM	Non-Cytosolic
263	U:414376.12:2001MAY17	580	602	forward 2	TM	Transmembrane
263	U:414376.12:2001MAY17	603	664	forward 2	TM	Cytosolic
263	U:414376.12:2001MAY17	665	687	forward 2	TM	Transmembrane
263	U:414376.12:2001MAY17	688	701	forward 2	TM	Non-Cytosolic
263	U:414376.12:2001MAY17	702	720	forward 2	TM	Transmembrane
263	U:414376.12:2001MAY17	721	726	forward 2	TM	Cytosolic
263	U:414376.12:2001MAY17	727	749	forward 2	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
263	U:414376.12:2001MAY17	750	1999	forward 2	TM	Non-Cytosolic
264	U:452089.1:2001MAY17	1	238	forward 1	TM	Non-Cytosolic
264	U:452089.1:2001MAY17	239	261	forward 1	TM	Transmembrane
264	U:452089.1:2001MAY17	262	312	forward 1	TM	Cytosolic
264	U:452089.1:2001MAY17	1	283	forward 2	TM	Non-Cytosolic
264	U:452089.1:2001MAY17	284	306	forward 2	TM	Transmembrane
264	U:452089.1:2001MAY17	307	312	forward 2	TM	Cytosolic
264	U:452089.1:2001MAY17	1	237	forward 3	TM	Cytosolic
264	U:452089.1:2001MAY17	238	260	forward 3	TM	Transmembrane
264	U:452089.1:2001MAY17	261	283	forward 3	TM	Non-Cytosolic
264	U:452089.1:2001MAY17	284	306	forward 3	TM	Transmembrane
264	U:452089.1:2001MAY17	307	311	forward 3	TM	Cytosolic
265	U:481614.43:2001MAY17	1	1525	forward 1	TM	Non-Cytosolic
265	U:481614.43:2001MAY17	1526	1548	forward 1	TM	Transmembrane
265	U:481614.43:2001MAY17	1549	1660	forward 1	TM	Cytosolic
266	U:809605.2:2001MAY17	1	81	forward 2	TM	Non-Cytosolic
266	U:809605.2:2001MAY17	82	104	forward 2	TM	Transmembrane
266	U:809605.2:2001MAY17	105	137	forward 2	TM	Cytosolic
266	U:809605.2:2001MAY17	138	160	forward 2	TM	Transmembrane
266	U:809605.2:2001MAY17	161	880	forward 2	TM	Non-Cytosolic
267	U:816437.25:2001MAY17	1	605	forward 1	TM	Non-Cytosolic
267	U:816437.25:2001MAY17	606	625	forward 1	TM	Transmembrane
267	U:816437.25:2001MAY17	626	679	forward 1	TM	Cytosolic
267	U:816437.25:2001MAY17	680	702	forward 1	TM	Transmembrane
267	U:816437.25:2001MAY17	703	859	forward 1	TM	Non-Cytosolic
267	U:816437.25:2001MAY17	860	882	forward 1	TM	Transmembrane
267	U:816437.25:2001MAY17	883	1250	forward 1	TM	Cytosolic
268	U:817827.5:2001MAY17	1	244	forward 1	TM	Non-Cytosolic
268	U:817827.5:2001MAY17	245	264	forward 1	TM	Transmembrane
268	U:817827.5:2001MAY17	265	272	forward 1	TM	Cytosolic
268	U:817827.5:2001MAY17	1	240	forward 2	TM	Non-Cytosolic
268	U:817827.5:2001MAY17	241	263	forward 2	TM	Transmembrane
268	U:817827.5:2001MAY17	264	271	forward 2	TM	Cytosolic
268	U:817827.5:2001MAY17	1	235	forward 3	TM	Non-Cytosolic
268	U:817827.5:2001MAY17	236	258	forward 3	TM	Transmembrane
268	U:817827.5:2001MAY17	259	271	forward 3	TM	Cytosolic
269	U:002345.15:2001MAY17	1	601	forward 1	TM	Non-Cytosolic
269	U:002345.15:2001MAY17	602	624	forward 1	TM	Transmembrane
269	U:002345.15:2001MAY17	625	946	forward 1	TM	Cytosolic
269	U:002345.15:2001MAY17	947	969	forward 1	TM	Transmembrane
269	U:002345.15:2001MAY17	970	1282	forward 1	TM	Non-Cytosolic
269	U:002345.15:2001MAY17	1283	1300	forward 1	TM	Transmembrane
269	U:002345.15:2001MAY17	1301	1307	forward 1	TM	Cytosolic
269	U:002345.15:2001MAY17	1	601	forward 2	TM	Non-Cytosolic
269	U:002345.15:2001MAY17	602	624	forward 2	TM	Transmembrane
269	U:002345.15:2001MAY17	625	636	forward 2	TM	Cytosolic
269	U:002345.15:2001MAY17	637	654	forward 2	TM	Transmembrane
269	U:002345.15:2001MAY17	655	663	forward 2	TM	Non-Cytosolic
269	U:002345.15:2001MAY17	664	681	forward 2	TM	Transmembrane
269	U:002345.15:2001MAY17	682	741	forward 2	TM	Cytosolic



TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
269	U:002345.15:2001MAY17	742	764	forward 2	TM	Transmembrane
269	U:002345.15:2001MAY17	765	814	forward 2	TM	Non-Cytosolic
269	U:002345.15:2001MAY17	815	837	forward 2	TM	Transmembrane
269	U:002345.15:2001MAY17	838	864	forward 2	TM	Cytosolic
269	U:002345.15:2001MAY17	865	887	forward 2	TM	Transmembrane
269	U:002345.15:2001MAY17	888	1117	forward 2	TM	Non-Cytosolic
269	U:002345.15:2001MAY17	1118	1140	forward 2	TM	Transmembrane
269	U:002345.15:2001MAY17	1141	1224	forward 2	TM	Cytosolic
269	U:002345.15:2001MAY17	1225	1247	forward 2	TM	Transmembrane
269	U:002345.15:2001MAY17	1248	1279	forward 2	TM	Non-Cytosolic
269	U:002345.15:2001MAY17	1280	1299	forward 2	TM	Transmembrane
269	U:002345.15:2001MAY17	1300	1307	forward 2	TM	Cytosolic
269	U:002345.15:2001MAY17	1	537	forward 3	TM	Non-Cytosolic
269	U:002345.15:2001MAY17	538	560	forward 3	TM	Transmembrane
269	U:002345.15:2001MAY17	561	598	forward 3	TM	Cytosolic
269	U:002345.15:2001MAY17	599	621	forward 3	TM	Transmembrane
269	U:002345.15:2001MAY17	622	625	forward 3	TM	Non-Cytosolic
269	U:002345.15:2001MAY17	626	648	forward 3	TM	Transmembrane
269	U:002345.15:2001MAY17	649	660	forward 3	TM	Cytosolic
269	U:002345.15:2001MAY17	661	678	forward 3	TM	Transmembrane
269	U:002345.15:2001MAY17	679	687	forward 3	TM	Non-Cytosolic
269	U:002345.15:2001MAY17	688	705	forward 3	TM	Transmembrane
269	U:002345.15:2001MAY17	706	798	forward 3	TM	Cytosolic
269	U:002345.15:2001MAY17	799	818	forward 3	TM	Transmembrane
269	U:002345.15:2001MAY17	819	822	forward 3	TM	Non-Cytosolic
269	U:002345.15:2001MAY17	823	845	forward 3	TM	Transmembrane
269	U:002345.15:2001MAY17	846	865	forward 3	TM	Cytosolic
269	U:002345.15:2001MAY17	866	888	forward 3	TM	Transmembrane
269	U:002345.15:2001MAY17	889	1307	forward 3	TM	Non-Cytosolic
270	U:022629.5:2001MAY17	1	92	forward 3	TM	Cytosolic
270	U:022629.5:2001MAY17	93	115	forward 3	TM	Transmembrane
270	U:022629.5:2001MAY17	116	139	forward 3	TM	Non-Cytosolic
270	U:022629.5:2001MAY17	140	162	forward 3	TM	Transmembrane
270	U:022629.5:2001MAY17	163	174	forward 3	TM	Cytosolic
270	U:022629.5:2001MAY17	175	197	forward 3	TM	Transmembrane
270	U:022629.5:2001MAY17	198	200	forward 3	TM	Non-Cytosolic
270	U:022629.5:2001MAY17	201	223	forward 3	TM	Transmembrane
270	U:022629.5:2001MAY17	224	312	forward 3	TM	Cytosolic
271	U:061031.4:2001MAY17	1	578	forward 1	TM	Non-Cytosolic
271	U:061031.4:2001MAY17	579	601	forward 1	TM	Transmembrane
271	U:061031.4:2001MAY17	602	688	forward 1	TM	Cytosolic
271	U:061031.4:2001MAY17	689	711	forward 1	TM	Transmembrane
271	U:061031.4:2001MAY17	712	745	forward 1	TM	Non-Cytosolic
271	U:061031.4:2001MAY17	746	768	forward 1	TM	Transmembrane
271	U:061031.4:2001MAY17	769	903	forward 1	TM	Cytosolic
271	U:061031.4:2001MAY17	1	120	forward 2	TM	Non-Cytosolic
271	U:061031.4:2001MAY17	121	140	forward 2	TM	Transmembrane
271	U:061031.4:2001MAY17	141	217	forward 2	TM	Cytosolic
271	U:061031.4:2001MAY17	218	240	forward 2	TM	Transmembrane
271	U:061031.4:2001MAY17	241	903	forward 2	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
272	U:108232.2:2001MAY17	1	20	forward 1	TM	Cytosolic
272	U:108232.2:2001MAY17	21	40	forward 1	TM	Transmembrane
272	U:108232.2:2001MAY17	41	54	forward 1	TM	Non-Cytosolic
272	U:108232.2:2001MAY17	55	77	forward 1	TM	Transmembrane
272	U:108232.2:2001MAY17	78	311	forward 1	TM	Cytosolic
273	U:1085493.16:2001MAY17	1	342	forward 2	TM	Cytosolic
273	U:1085493.16:2001MAY17	343	365	forward 2	TM	Transmembrane
273	U:1085493.16:2001MAY17	366	384	forward 2	TM	Non-Cytosolic
273	U:1085493.16:2001MAY17	385	403	forward 2	TM	Transmembrane
273	U:1085493.16:2001MAY17	404	498	forward 2	TM	Cytosolic
273	U:1085493.16:2001MAY17	499	521	forward 2	TM	Transmembrane
273	U:1085493.16:2001MAY17	522	1015	forward 2	TM	Non-Cytosolic
273	U:1085493.16:2001MAY17	1	385	forward 3	TM	Non-Cytosolic
273	U:1085493.16:2001MAY17	386	408	forward 3	TM	Transmembrane
273	U:1085493.16:2001MAY17	409	517	forward 3	TM	Cytosolic
273	U:1085493.16:2001MAY17	518	540	forward 3	TM	Transmembrane
273	U:1085493.16:2001MAY17	541	1015	forward 3	TM	Non-Cytosolic
274	U:1085513.2:2001MAY17	1	722	forward 1	TM	Non-Cytosolic
274	U:1085513.2:2001MAY17	723	745	forward 1	TM	Transmembrane
274	U:1085513.2:2001MAY17	746	757	forward 1	TM	Cytosolic
274	U:1085513.2:2001MAY17	758	780	forward 1	TM	Transmembrane
274	U:1085513.2:2001MAY17	781	838	forward 1	TM	Non-Cytosolic
274	U:1085513.2:2001MAY17	839	861	forward 1	TM	Transmembrane
274	U:1085513.2:2001MAY17	862	896	forward 1	TM	Cytosolic
274	U:1085513.2:2001MAY17	1	639	forward 2	TM	Non-Cytosolic
274	U:1085513.2:2001MAY17	640	662	forward 2	TM	Transmembrane
274	U:1085513.2:2001MAY17	663	730	forward 2	TM	Cytosolic
274	U:1085513.2:2001MAY17	731	753	forward 2	TM	Transmembrane
274	U:1085513.2:2001MAY17	754	767	forward 2	TM	Non-Cytosolic
274	U:1085513.2:2001MAY17	768	790	forward 2	TM	Transmembrane
274	U:1085513.2:2001MAY17	791	895	forward 2	TM	Cytosolic
274	U:1085513.2:2001MAY17	1	151	forward 3	TM	Non-Cytosolic
274	U:1085513.2:2001MAY17	152	171	forward 3	TM	Transmembrane
274	U:1085513.2:2001MAY17	172	177	forward 3	TM	Cytosolic
274	U:1085513.2:2001MAY17	178	200	forward 3	TM	Transmembrane
274	U:1085513.2:2001MAY17	201	203	forward 3	TM	Non-Cytosolic
274	U:1085513.2:2001MAY17	204	226	forward 3	TM	Transmembrane
274	U:1085513.2:2001MAY17	227	237	forward 3	TM	Cytosolic
274	U:1085513.2:2001MAY17	238	257	forward 3	TM	Transmembrane
274	U:1085513.2:2001MAY17	258	271	forward 3	TM	Non-Cytosolic
274	U:1085513.2:2001MAY17	272	294	forward 3	TM	Transmembrane
274	U:1085513.2:2001MAY17	295	298	forward 3	TM	Cytosolic
274	U:1085513.2:2001MAY17	299	321	forward 3	TM	Transmembrane
274	U:1085513.2:2001MAY17	322	370	forward 3	TM	Non-Cytosolic
274	U:1085513.2:2001MAY17	371	393	forward 3	TM	Transmembrane
274	U:1085513.2:2001MAY17	394	405	forward 3	TM	Cytosolic
274	U:1085513.2:2001MAY17	406	439	forward 3	TM	Transmembrane
274	U:1085513.2:2001MAY17	440	453	forward 3	TM	Non-Cytosolic
274	U:1085513.2:2001MAY17	454	476	forward 3	TM	Transmembrane
274	U:1085513.2:2001MAY17	477	482	forward 3	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
274	U:1085513.2:2001MAY17	483	505	forward 3	TM	Transmembrane
274	U:1085513.2:2001MAY17	506	554	forward 3	TM	Non-Cytosolic
274	U:1085513.2:2001MAY17	555	577	forward 3	TM	Transmembrane
274	U:1085513.2:2001MAY17	578	647	forward 3	TM	Cytosolic
274	U:1085513.2:2001MAY17	648	670	forward 3	TM	Transmembrane
274	U:1085513.2:2001MAY17	671	702	forward 3	TM	Non-Cytosolic
274	U:1085513.2:2001MAY17	703	725	forward 3	TM	Transmembrane
274	U:1085513.2:2001MAY17	726	736	forward 3	TM	Cytosolic
274	U:1085513.2:2001MAY17	737	759	forward 3	TM	Transmembrane
274	U:1085513.2:2001MAY17	760	895	forward 3	TM	Non-Cytosolic
275	U:1086797.9:2001MAY17	1	57	forward 1	TM	Cytosolic
275	U:1086797.9:2001MAY17	58	80	forward 1	TM	Transmembrane
275	U:1086797.9:2001MAY17	81	894	forward 1	TM	Non-Cytosolic
275	U:1086797.9:2001MAY17	895	917	forward 1	TM	Transmembrane
275	U:1086797.9:2001MAY17	918	988	forward 1	TM	Cytosolic
275	U:1086797.9:2001MAY17	989	1011	forward 1	TM	Transmembrane
275	U:1086797.9:2001MAY17	1012	2215	forward 1	TM	Non-Cytosolic
275	U:1086797.9:2001MAY17	1	19	forward 2	TM	Cytosolic
275	U:1086797.9:2001MAY17	20	42	forward 2	TM	Transmembrane
275	U:1086797.9:2001MAY17	43	61	forward 2	TM	Non-Cytosolic
275	U:1086797.9:2001MAY17	62	84	forward 2	TM	Transmembrane
275	U:1086797.9:2001MAY17	85	618	forward 2	TM	Cytosolic
275	U:1086797.9:2001MAY17	619	641	forward 2	TM	Transmembrane
275	U:1086797.9:2001MAY17	642	2214	forward 2	TM	Non-Cytosolic
275	U:1086797.9:2001MAY17	1	23	forward 3	TM	Non-Cytosolic
275	U:1086797.9:2001MAY17	24	46	forward 3	TM	Transmembrane
275	U:1086797.9:2001MAY17	47	58	forward 3	TM	Cytosolic
275	U:1086797.9:2001MAY17	59	81	forward 3	TM	Transmembrane
275	U:1086797.9:2001MAY17	82	1567	forward 3	TM	Non-Cytosolic
275	U:1086797.9:2001MAY17	1568	1590	forward 3	TM	Transmembrane
275	U:1086797.9:2001MAY17	1591	1591	forward 3	TM	Cytosolic
275	U:1086797.9:2001MAY17	1592	1614	forward 3	TM	Transmembrane
275	U:1086797.9:2001MAY17	1615	2117	forward 3	TM	Non-Cytosolic
275	U:1086797.9:2001MAY17	2118	2140	forward 3	TM	Transmembrane
275	U:1086797.9:2001MAY17	2141	2214	forward 3	TM	Cytosolic
276	U:1088446.1:2001MAY17	1	429	forward 1	TM	Non-Cytosolic
276	U:1088446.1:2001MAY17	430	449	forward 1	TM	Transmembrane
276	U:1088446.1:2001MAY17	450	593	forward 1	TM	Cytosolic
276	U:1088446.1:2001MAY17	594	616	forward 1	TM	Transmembrane
276	U:1088446.1:2001MAY17	617	828	forward 1	TM	Non-Cytosolic
277	U:1133764.3:2001MAY17	1	560	forward 3	TM	Non-Cytosolic
277	U:1133764.3:2001MAY17	561	583	forward 3	TM	Transmembrane
277	U:1133764.3:2001MAY17	584	643	forward 3	TM	Cytosolic
277	U:1133764.3:2001MAY17	644	666	forward 3	TM	Transmembrane
277	U:1133764.3:2001MAY17	667	766	forward 3	TM	Non-Cytosolic
278	U:1147614.5:2001MAY17	1	12	forward 3	TM	Cytosolic
278	U:1147614.5:2001MAY17	13	35	forward 3	TM	Transmembrane
278	U:1147614.5:2001MAY17	36	1045	forward 3	TM	Non-Cytosolic
279	U:1181710.1:2001MAY17	1	95	forward 2	TM	Cytosolic
279	U:1181710.1:2001MAY17	96	118	forward 2	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
279	U:1181710.1:2001MAY17	119	222	forward 2	TM	Non-Cytosolic
280	U:1183192.1:2001MAY17	1	403	forward 2	TM	Non-Cytosolic
280	U:1183192.1:2001MAY17	404	426	forward 2	TM	Transmembrane
280	U:1183192.1:2001MAY17	427	529	forward 2	TM	Cytosolic
281	U:1188786.15:2001MAY17	1	615	forward 1	TM	Non-Cytosolic
281	U:1188786.15:2001MAY17	616	638	forward 1	TM	Transmembrane
281	U:1188786.15:2001MAY17	639	736	forward 1	TM	Cytosolic
281	U:1188786.15:2001MAY17	737	759	forward 1	TM	Transmembrane
281	U:1188786.15:2001MAY17	760	841	forward 1	TM	Non-Cytosolic
281	U:1188786.15:2001MAY17	842	864	forward 1	TM	Transmembrane
281	U:1188786.15:2001MAY17	865	1114	forward 1	TM	Cytosolic
281	U:1188786.15:2001MAY17	1115	1137	forward 1	TM	Transmembrane
281	U:1188786.15:2001MAY17	1138	1207	forward 1	TM	Non-Cytosolic
281	U:1188786.15:2001MAY17	1208	1230	forward 1	TM	Transmembrane
281	U:1188786.15:2001MAY17	1231	1253	forward 1	TM	Cytosolic
281	U:1188786.15:2001MAY17	1	589	forward 2	TM	Non-Cytosolic
281	U:1188786.15:2001MAY17	590	609	forward 2	TM	Transmembrane
281	U:1188786.15:2001MAY17	610	615	forward 2	TM	Cytosolic
281	U:1188786.15:2001MAY17	616	638	forward 2	TM	Transmembrane
281	U:1188786.15:2001MAY17	639	669	forward 2	TM	Non-Cytosolic
281	U:1188786.15:2001MAY17	670	692	forward 2	TM	Transmembrane
281	U:1188786.15:2001MAY17	693	698	forward 2	TM	Cytosolic
281	U:1188786.15:2001MAY17	699	721	forward 2	TM	Transmembrane
281	U:1188786.15:2001MAY17	722	735	forward 2	TM	Non-Cytosolic
281	U:1188786.15:2001MAY17	736	754	forward 2	TM	Transmembrane
281	U:1188786.15:2001MAY17	755	924	forward 2	TM	Cytosolic
281	U:1188786.15:2001MAY17	925	947	forward 2	TM	Transmembrane
281	U:1188786.15:2001MAY17	948	1002	forward 2	TM	Non-Cytosolic
281	U:1188786.15:2001MAY17	1003	1025	forward 2	TM	Transmembrane
281	U:1188786.15:2001MAY17	1026	1044	forward 2	TM	Cytosolic
281	U:1188786.15:2001MAY17	1045	1067	forward 2	TM	Transmembrane
281	U:1188786.15:2001MAY17	1068	1213	forward 2	TM	Non-Cytosolic
281	U:1188786.15:2001MAY17	1214	1236	forward 2	TM	Transmembrane
281	U:1188786.15:2001MAY17	1237	1253	forward 2	TM	Cytosolic
281	U:1188786.15:2001MAY17	1	65	forward 3	TM	Cytosolic
281	U:1188786.15:2001MAY17	66	88	forward 3	TM	Transmembrane
281	U:1188786.15:2001MAY17	89	568	forward 3	TM	Non-Cytosolic
281	U:1188786.15:2001MAY17	569	587	forward 3	TM	Transmembrane
281	U:1188786.15:2001MAY17	588	617	forward 3	TM	Cytosolic
281	U:1188786.15:2001MAY17	618	640	forward 3	TM	Transmembrane
281	U:1188786.15:2001MAY17	641	666	forward 3	TM	Non-Cytosolic
281	U:1188786.15:2001MAY17	667	689	forward 3	TM	Transmembrane
281	U:1188786.15:2001MAY17	690	701	forward 3	TM	Cytosolic
281	U:1188786.15:2001MAY17	702	721	forward 3	TM	Transmembrane
281	U:1188786.15:2001MAY17	722	735	forward 3	TM	Non-Cytosolic
281	U:1188786.15:2001MAY17	736	758	forward 3	TM	Transmembrane
281	U:1188786.15:2001MAY17	759	802	forward 3	TM	Cytosolic
281	U:1188786.15:2001MAY17	803	825	forward 3	TM	Transmembrane
281	U:1188786.15:2001MAY17	826	924	forward 3	TM	Non-Cytosolic
281	U:1188786.15:2001MAY17	925	947	forward 3	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
281	U:1188786.15:2001MAY17	948	1041	forward 3	TM	Cytosolic
281	U:1188786.15:2001MAY17	1042	1064	forward 3	TM	Transmembrane
281	U:1188786.15:2001MAY17	1065	1093	forward 3	TM	Non-Cytosolic
281	U:1188786.15:2001MAY17	1094	1116	forward 3	TM	Transmembrane
281	U:1188786.15:2001MAY17	1117	1253	forward 3	TM	Cytosolic
282	U:145626.1:2001MAY17	1	662	forward 2	TM	Non-Cytosolic
282	U:145626.1:2001MAY17	663	685	forward 2	TM	Transmembrane
282	U:145626.1:2001MAY17	686	947	forward 2	TM	Cytosolic
282	U:145626.1:2001MAY17	948	970	forward 2	TM	Transmembrane
282	U:145626.1:2001MAY17	971	1038	forward 2	TM	Non-Cytosolic
283	U:147869.3:2001MAY17	1	94	forward 1	TM	Cytosolic
283	U:147869.3:2001MAY17	95	117	forward 1	TM	Transmembrane
283	U:147869.3:2001MAY17	118	131	forward 1	TM	Non-Cytosolic
283	U:147869.3:2001MAY17	132	154	forward 1	TM	Transmembrane
283	U:147869.3:2001MAY17	155	221	forward 1	TM	Cytosolic
283	U:147869.3:2001MAY17	222	244	forward 1	TM	Transmembrane
283	U:147869.3:2001MAY17	245	419	forward 1	TM	Non-Cytosolic
283	U:147869.3:2001MAY17	420	442	forward 1	TM	Transmembrane
283	U:147869.3:2001MAY17	443	446	forward 1	TM	Cytosolic
283	U:147869.3:2001MAY17	447	469	forward 1	TM	Transmembrane
283	U:147869.3:2001MAY17	470	478	forward 1	TM	Non-Cytosolic
283	U:147869.3:2001MAY17	479	501	forward 1	TM	Transmembrane
283	U:147869.3:2001MAY17	502	513	forward 1	TM	Cytosolic
283	U:147869.3:2001MAY17	514	536	forward 1	TM	Transmembrane
283	U:147869.3:2001MAY17	537	550	forward 1	TM	Non-Cytosolic
283	U:147869.3:2001MAY17	551	573	forward 1	TM	Transmembrane
283	U:147869.3:2001MAY17	574	619	forward 1	TM	Cytosolic
283	U:147869.3:2001MAY17	1	470	forward 2	TM	Non-Cytosolic
283	U:147869.3:2001MAY17	471	493	forward 2	TM	Transmembrane
283	U:147869.3:2001MAY17	494	519	forward 2	TM	Cytosolic
283	U:147869.3:2001MAY17	520	542	forward 2	TM	Transmembrane
283	U:147869.3:2001MAY17	543	551	forward 2	TM	Non-Cytosolic
283	U:147869.3:2001MAY17	552	571	forward 2	TM	Transmembrane
283	U:147869.3:2001MAY17	572	591	forward 2	TM	Cytosolic
283	U:147869.3:2001MAY17	592	614	forward 2	TM	Transmembrane
283	U:147869.3:2001MAY17	615	619	forward 2	TM	Non-Cytosolic
284	U:151747.4:2001MAY17	1	671	forward 1	TM	Non-Cytosolic
284	U:151747.4:2001MAY17	672	691	forward 1	TM	Transmembrane
284	U:151747.4:2001MAY17	692	860	forward 1	TM	Cytosolic
284	U:151747.4:2001MAY17	861	883	forward 1	TM	Transmembrane
284	U:151747.4:2001MAY17	884	897	forward 1	TM	Non-Cytosolic
284	U:151747.4:2001MAY17	898	920	forward 1	TM	Transmembrane
284	U:151747.4:2001MAY17	921	1133	forward 1	TM	Cytosolic
284	U:151747.4:2001MAY17	1134	1156	forward 1	TM	Transmembrane
284	U:151747.4:2001MAY17	1157	1209	forward 1	TM	Non-Cytosolic
284	U:151747.4:2001MAY17	1210	1232	forward 1	TM	Transmembrane
284	U:151747.4:2001MAY17	1233	1238	forward 1	TM	Cytosolic
284	U:151747.4:2001MAY17	1239	1258	forward 1	TM	Transmembrane
284	U:151747.4:2001MAY17	1259	1272	forward 1	TM	Non-Cytosolic
284	U:151747.4:2001MAY17	1273	1295	forward 1	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
284	U:151747.4:2001MAY17	1296	1299	forward 1	TM	Cytosolic
284	U:151747.4:2001MAY17	1300	1322	forward 1	TM	Transmembrane
284	U:151747.4:2001MAY17	1323	1366	forward 1	TM	Non-Cytosolic
284	U:151747.4:2001MAY17	1367	1386	forward 1	TM	Transmembrane
284	U:151747.4:2001MAY17	1387	1392	forward 1	TM	Cytosolic
284	U:151747.4:2001MAY17	1393	1415	forward 1	TM	Transmembrane
284	U:151747.4:2001MAY17	1416	1434	forward 1	TM	Non-Cytosolic
284	U:151747.4:2001MAY17	1435	1457	forward 1	TM	Transmembrane
284	U:151747.4:2001MAY17	1458	1535	forward 1	TM	Cytosolic
284	U:151747.4:2001MAY17	1	532	forward 2	TM	Non-Cytosolic
284	U:151747.4:2001MAY17	533	555	forward 2	TM	Transmembrane
284	U:151747.4:2001MAY17	556	575	forward 2	TM	Cytosolic
284	U:151747.4:2001MAY17	576	598	forward 2	TM	Transmembrane
284	U:151747.4:2001MAY17	599	673	forward 2	TM	Non-Cytosolic
284	U:151747.4:2001MAY17	674	693	forward 2	TM	Transmembrane
284	U:151747.4:2001MAY17	694	845	forward 2	TM	Cytosolic
284	U:151747.4:2001MAY17	846	865	forward 2	TM	Transmembrane
284	U:151747.4:2001MAY17	866	896	forward 2	TM	Non-Cytosolic
284	U:151747.4:2001MAY17	897	919	forward 2	TM	Transmembrane
284	U:151747.4:2001MAY17	920	976	forward 2	TM	Cytosolic
284	U:151747.4:2001MAY17	977	999	forward 2	TM	Transmembrane
284	U:151747.4:2001MAY17	1000	1085	forward 2	TM	Non-Cytosolic
284	U:151747.4:2001MAY17	1086	1108	forward 2	TM	Transmembrane
284	U:151747.4:2001MAY17	1109	1206	forward 2	TM	Cytosolic
284	U:151747.4:2001MAY17	1207	1229	forward 2	TM	Transmembrane
284	U:151747.4:2001MAY17	1230	1238	forward 2	TM	Non-Cytosolic
284	U:151747.4:2001MAY17	1239	1258	forward 2	TM	Transmembrane
284	U:151747.4:2001MAY17	1259	1327	forward 2	TM	Cytosolic
284	U:151747.4:2001MAY17	1328	1350	forward 2	TM	Transmembrane
284	U:151747.4:2001MAY17	1351	1372	forward 2	TM	Non-Cytosolic
284	U:151747.4:2001MAY17	1373	1395	forward 2	TM	Transmembrane
284	U:151747.4:2001MAY17	1396	1401	forward 2	TM	Cytosolic
284	U:151747.4:2001MAY17	1402	1424	forward 2	TM	Transmembrane
284	U:151747.4:2001MAY17	1425	1438	forward 2	TM	Non-Cytosolic
284	U:151747.4:2001MAY17	1439	1461	forward 2	TM	Transmembrane
284	U:151747.4:2001MAY17	1462	1535	forward 2	TM	Cytosolic
284	U:151747.4:2001MAY17	1	660	forward 3	TM	Non-Cytosolic
284	U:151747.4:2001MAY17	661	683	forward 3	TM	Transmembrane
284	U:151747.4:2001MAY17	684	857	forward 3	TM	Cytosolic
284	U:151747.4:2001MAY17	858	880	forward 3	TM	Transmembrane
284	U:151747.4:2001MAY17	881	889	forward 3	TM	Non-Cytosolic
284	U:151747.4:2001MAY17	890	912	forward 3	TM	Transmembrane
284	U:151747.4:2001MAY17	913	1000	forward 3	TM	Cytosolic
284	U:151747.4:2001MAY17	1001	1020	forward 3	TM	Transmembrane
284	U:151747.4:2001MAY17	1021	1029	forward 3	TM	Non-Cytosolic
284	U:151747.4:2001MAY17	1030	1047	forward 3	TM	Transmembrane
284	U:151747.4:2001MAY17	1048	1085	forward 3	TM	Cytosolic
284	U:151747.4:2001MAY17	1086	1108	forward 3	TM	Transmembrane
284	U:151747.4:2001MAY17	1109	1120	forward 3	TM	Non-Cytosolic
284	U:151747.4:2001MAY17	1121	1143	forward 3	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
284	U:151747.4:2001MAY17	1144	1204	forward 3	TM	Cytosolic
284	U:151747.4:2001MAY17	1205	1227	forward 3	TM	Transmembrane
284	U:151747.4:2001MAY17	1228	1292	forward 3	TM	Non-Cytosolic
284	U:151747.4:2001MAY17	1293	1315	forward 3	TM	Transmembrane
284	U:151747.4:2001MAY17	1316	1327	forward 3	TM	Cytosolic
284	U:151747.4:2001MAY17	1328	1350	forward 3	TM	Transmembrane
284	U:151747.4:2001MAY17	1351	1375	forward 3	TM	Non-Cytosolic
284	U:151747.4:2001MAY17	1376	1398	forward 3	TM	Transmembrane
284	U:151747.4:2001MAY17	1399	1404	forward 3	TM	Cytosolic
284	U:151747.4:2001MAY17	1405	1427	forward 3	TM	Transmembrane
284	U:151747.4:2001MAY17	1428	1441	forward 3	TM	Non-Cytosolic
284	U:151747.4:2001MAY17	1442	1464	forward 3	TM	Transmembrane
284	U:151747.4:2001MAY17	1465	1470	forward 3	TM	Cytosolic
284	U:151747.4:2001MAY17	1471	1493	forward 3	TM	Transmembrane
284	U:151747.4:2001MAY17	1494	1535	forward 3	TM	Non-Cytosolic
285	U:198296.1:2001MAY17	1	896	forward 1	TM	Non-Cytosolic
285	U:198296.1:2001MAY17	897	914	forward 1	TM	Transmembrane
285	U:198296.1:2001MAY17	915	920	forward 1	TM	Cytosolic
285	U:198296.1:2001MAY17	921	943	forward 1	TM	Transmembrane
285	U:198296.1:2001MAY17	944	1036	forward 1	TM	Non-Cytosolic
285	U:198296.1:2001MAY17	1037	1059	forward 1	TM	Transmembrane
285	U:198296.1:2001MAY17	1060	1127	forward 1	TM	Cytosolic
285	U:198296.1:2001MAY17	1128	1150	forward 1	TM	Transmembrane
285	U:198296.1:2001MAY17	1151	1176	forward 1	TM	Non-Cytosolic
285	U:198296.1:2001MAY17	1177	1199	forward 1	TM	Transmembrane
285	U:198296.1:2001MAY17	1200	1211	forward 1	TM	Cytosolic
285	U:198296.1:2001MAY17	1212	1234	forward 1	TM	Transmembrane
285	U:198296.1:2001MAY17	1235	1286	forward 1	TM	Non-Cytosolic
285	U:198296.1:2001MAY17	1287	1309	forward 1	TM	Transmembrane
285	U:198296.1:2001MAY17	1310	1329	forward 1	TM	Cytosolic
285	U:198296.1:2001MAY17	1330	1352	forward 1	TM	Transmembrane
285	U:198296.1:2001MAY17	1353	1428	forward 1	TM	Non-Cytosolic
285	U:198296.1:2001MAY17	1429	1451	forward 1	TM	Transmembrane
285	U:198296.1:2001MAY17	1452	1456	forward 1	TM	Cytosolic
285	U:198296.1:2001MAY17	1	20	forward 2	TM	Cytosolic
285	U:198296.1:2001MAY17	21	43	forward 2	TM	Transmembrane
285	U:198296.1:2001MAY17	44	530	forward 2	TM	Non-Cytosolic
285	U:198296.1:2001MAY17	531	553	forward 2	TM	Transmembrane
285	U:198296.1:2001MAY17	554	573	forward 2	TM	Cytosolic
285	U:198296.1:2001MAY17	574	596	forward 2	TM	Transmembrane
285	U:198296.1:2001MAY17	597	605	forward 2	TM	Non-Cytosolic
285	U:198296.1:2001MAY17	606	628	forward 2	TM	Transmembrane
285	U:198296.1:2001MAY17	629	766	forward 2	TM	Cytosolic
285	U:198296.1:2001MAY17	767	789	forward 2	TM	Transmembrane
285	U:198296.1:2001MAY17	790	813	forward 2	TM	Non-Cytosolic
285	U:198296.1:2001MAY17	814	836	forward 2	TM	Transmembrane
285	U:198296.1:2001MAY17	837	1054	forward 2	TM	Cytosolic
285	U:198296.1:2001MAY17	1055	1077	forward 2	TM	Transmembrane
285	U:198296.1:2001MAY17	1078	1091	forward 2	TM	Non-Cytosolic
285	U:198296.1:2001MAY17	1092	1114	forward 2	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
285	U:198296.1:2001MAY17	1115	1126	forward 2	TM	Cytosolic
285	U:198296.1:2001MAY17	1127	1149	forward 2	TM	Transmembrane
285	U:198296.1:2001MAY17	1150	1216	forward 2	TM	Non-Cytosolic
285	U:198296.1:2001MAY17	1217	1239	forward 2	TM	Transmembrane
285	U:198296.1:2001MAY17	1240	1285	forward 2	TM	Cytosolic
285	U:198296.1:2001MAY17	1286	1308	forward 2	TM	Transmembrane
285	U:198296.1:2001MAY17	1309	1339	forward 2	TM	Non-Cytosolic
285	U:198296.1:2001MAY17	1340	1362	forward 2	TM	Transmembrane
285	U:198296.1:2001MAY17	1363	1405	forward 2	TM	Cytosolic
285	U:198296.1:2001MAY17	1406	1425	forward 2	TM	Transmembrane
285	U:198296.1:2001MAY17	1426	1456	forward 2	TM	Non-Cytosolic
285	U:198296.1:2001MAY17	1	458	forward 3	TM	Non-Cytosolic
285	U:198296.1:2001MAY17	459	481	forward 3	TM	Transmembrane
285	U:198296.1:2001MAY17	482	524	forward 3	TM	Cytosolic
285	U:198296.1:2001MAY17	525	547	forward 3	TM	Transmembrane
285	U:198296.1:2001MAY17	548	921	forward 3	TM	Non-Cytosolic
285	U:198296.1:2001MAY17	922	944	forward 3	TM	Transmembrane
285	U:198296.1:2001MAY17	945	1010	forward 3	TM	Cytosolic
285	U:198296.1:2001MAY17	1011	1028	forward 3	TM	Transmembrane
285	U:198296.1:2001MAY17	1029	1136	forward 3	TM	Non-Cytosolic
285	U:198296.1:2001MAY17	1137	1159	forward 3	TM	Transmembrane
285	U:198296.1:2001MAY17	1160	1219	forward 3	TM	Cytosolic
285	U:198296.1:2001MAY17	1220	1242	forward 3	TM	Transmembrane
285	U:198296.1:2001MAY17	1243	1274	forward 3	TM	Non-Cytosolic
285	U:198296.1:2001MAY17	1275	1297	forward 3	TM	Transmembrane
285	U:198296.1:2001MAY17	1298	1405	forward 3	TM	Cytosolic
285	U:198296.1:2001MAY17	1406	1425	forward 3	TM	Transmembrane
285	U:198296.1:2001MAY17	1426	1456	forward 3	TM	Non-Cytosolic
286	U:200117.4:2001MAY17	1	338	forward 1	TM	Non-Cytosolic
286	U:200117.4:2001MAY17	339	361	forward 1	TM	Transmembrane
286	U:200117.4:2001MAY17	362	381	forward 1	TM	Cytosolic
286	U:200117.4:2001MAY17	382	399	forward 1	TM	Transmembrane
286	U:200117.4:2001MAY17	400	441	forward 1	TM	Non-Cytosolic
287	U:200704.1:2001MAY17	1	28	forward 1	TM	Cytosolic
287	U:200704.1:2001MAY17	29	51	forward 1	TM	Transmembrane
287	U:200704.1:2001MAY17	52	880	forward 1	TM	Non-Cytosolic
287	U:200704.1:2001MAY17	1	571	forward 3	TM	Non-Cytosolic
287	U:200704.1:2001MAY17	572	594	forward 3	TM	Transmembrane
287	U:200704.1:2001MAY17	595	705	forward 3	TM	Cytosolic
287	U:200704.1:2001MAY17	706	728	forward 3	TM	Transmembrane
287	U:200704.1:2001MAY17	729	772	forward 3	TM	Non-Cytosolic
287	U:200704.1:2001MAY17	773	792	forward 3	TM	Transmembrane
287	U:200704.1:2001MAY17	793	879	forward 3	TM	Cytosolic
288	U:2049995.3:2001MAY17	1	1134	forward 1	TM	Non-Cytosolic
288	U:2049995.3:2001MAY17	1135	1157	forward 1	TM	Transmembrane
288	U:2049995.3:2001MAY17	1158	1217	forward 1	TM	Cytosolic
288	U:2049995.3:2001MAY17	1218	1240	forward 1	TM	Transmembrane
288	U:2049995.3:2001MAY17	1241	1276	forward 1	TM	Non-Cytosolic
288	U:2049995.3:2001MAY17	1277	1295	forward 1	TM	Transmembrane
288	U:2049995.3:2001MAY17	1296	1453	forward 1	TM	Cytosolic



TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
288	U:2049995.3:2001MAY17	1454	1476	forward 1	TM	Transmembrane
288	U:2049995.3:2001MAY17	1477	1504	forward 1	TM	Non-Cytosolic
288	U:2049995.3:2001MAY17	1505	1527	forward 1	TM	Transmembrane
288	U:2049995.3:2001MAY17	1528	1642	forward 1	TM	Cytosolic
288	U:2049995.3:2001MAY17	1643	1660	forward 1	TM	Transmembrane
288	U:2049995.3:2001MAY17	1661	1668	forward 1	TM	Non-Cytosolic
288	U:2049995.3:2001MAY17	1	831	forward 2	TM	Non-Cytosolic
288	U:2049995.3:2001MAY17	832	854	forward 2	TM	Transmembrane
288	U:2049995.3:2001MAY17	855	913	forward 2	TM	Cytosolic
288	U:2049995.3:2001MAY17	914	936	forward 2	TM	Transmembrane
288	U:2049995.3:2001MAY17	937	1061	forward 2	TM	Non-Cytosolic
288	U:2049995.3:2001MAY17	1062	1084	forward 2	TM	Transmembrane
288	U:2049995.3:2001MAY17	1085	1096	forward 2	TM	Cytosolic
288	U:2049995.3:2001MAY17	1097	1119	forward 2	TM	Transmembrane
288	U:2049995.3:2001MAY17	1120	1122	forward 2	TM	Non-Cytosolic
288	U:2049995.3:2001MAY17	1123	1145	forward 2	TM	Transmembrane
288	U:2049995.3:2001MAY17	1146	1635	forward 2	TM	Cytosolic
288	U:2049995.3:2001MAY17	1636	1658	forward 2	TM	Transmembrane
288	U:2049995.3:2001MAY17	1659	1668	forward 2	TM	Non-Cytosolic
288	U:2049995.3:2001MAY17	1	1125	forward 3	TM	Non-Cytosolic
288	U:2049995.3:2001MAY17	1126	1148	forward 3	TM	Transmembrane
288	U:2049995.3:2001MAY17	1149	1263	forward 3	TM	Cytosolic
288	U:2049995.3:2001MAY17	1264	1283	forward 3	TM	Transmembrane
288	U:2049995.3:2001MAY17	1284	1302	forward 3	TM	Non-Cytosolic
288	U:2049995.3:2001MAY17	1303	1325	forward 3	TM	Transmembrane
288	U:2049995.3:2001MAY17	1326	1448	forward 3	TM	Cytosolic
288	U:2049995.3:2001MAY17	1449	1471	forward 3	TM	Transmembrane
288	U:2049995.3:2001MAY17	1472	1667	forward 3	TM	Non-Cytosolic
289	U:2052097.2:2001MAY17	1	939	forward 3	TM	Non-Cytosolic
289	U:2052097.2:2001MAY17	940	962	forward 3	TM	Transmembrane
289	U:2052097.2:2001MAY17	963	982	forward 3	TM	Cytosolic
289	U:2052097.2:2001MAY17	983	1005	forward 3	TM	Transmembrane
289	U:2052097.2:2001MAY17	1006	1008	forward 3	TM	Non-Cytosolic
289	U:2052097.2:2001MAY17	1009	1031	forward 3	TM	Transmembrane
289	U:2052097.2:2001MAY17	1032	1062	forward 3	TM	Cytosolic
290	U:209351.22:2001MAY17	1	845	forward 2	TM	Non-Cytosolic
290	U:209351.22:2001MAY17	846	868	forward 2	TM	Transmembrane
290	U:209351.22:2001MAY17	869	922	forward 2	TM	Cytosolic
290	U:209351.22:2001MAY17	1	730	forward 3	TM	Non-Cytosolic
290	U:209351.22:2001MAY17	731	753	forward 3	TM	Transmembrane
290	U:209351.22:2001MAY17	754	853	forward 3	TM	Cytosolic
290	U:209351.22:2001MAY17	854	876	forward 3	TM	Transmembrane
290	U:209351.22:2001MAY17	877	922	forward 3	TM	Non-Cytosolic
291	U:2120481.1:2001MAY17	1	218	forward 1	TM	Non-Cytosolic
291	U:2120481.1:2001MAY17	219	241	forward 1	TM	Transmembrane
291	U:2120481.1:2001MAY17	242	252	forward 1	TM	Cytosolic
291	U:2120481.1:2001MAY17	253	275	forward 1	TM	Transmembrane
291	U:2120481.1:2001MAY17	276	284	forward 1	TM	Non-Cytosolic
291	U:2120481.1:2001MAY17	285	304	forward 1	TM	Transmembrane
291	U:2120481.1:2001MAY17	305	344	forward 1	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
291	U:2120481.1:2001MAY17	345	367	forward 1	TM	Transmembrane
291	U:2120481.1:2001MAY17	368	386	forward 1	TM	Non-Cytosolic
291	U:2120481.1:2001MAY17	387	409	forward 1	TM	Transmembrane
291	U:2120481.1:2001MAY17	410	461	forward 1	TM	Cytosolic
291	U:2120481.1:2001MAY17	462	484	forward 1	TM	Transmembrane
291	U:2120481.1:2001MAY17	485	493	forward 1	TM	Non-Cytosolic
291	U:2120481.1:2001MAY17	494	516	forward 1	TM	Transmembrane
291	U:2120481.1:2001MAY17	517	527	forward 1	TM	Cytosolic
291	U:2120481.1:2001MAY17	528	550	forward 1	TM	Transmembrane
291	U:2120481.1:2001MAY17	551	551	forward 1	TM	Non-Cytosolic
291	U:2120481.1:2001MAY17	1	522	forward 2	TM	Non-Cytosolic
291	U:2120481.1:2001MAY17	523	545	forward 2	TM	Transmembrane
291	U:2120481.1:2001MAY17	546	551	forward 2	TM	Cytosolic
292	U:2121610.13:2001MAY17	1	6	forward 1	TM	Cytosolic
292	U:2121610.13:2001MAY17	7	29	forward 1	TM	Transmembrane
292	U:2121610.13:2001MAY17	30	316	forward 1	TM	Non-Cytosolic
292	U:2121610.13:2001MAY17	1	77	forward 3	TM	Non-Cytosolic
292	U:2121610.13:2001MAY17	78	100	forward 3	TM	Transmembrane
292	U:2121610.13:2001MAY17	101	140	forward 3	TM	Cytosolic
292	U:2121610.13:2001MAY17	141	163	forward 3	TM	Transmembrane
292	U:2121610.13:2001MAY17	164	177	forward 3	TM	Non-Cytosolic
292	U:2121610.13:2001MAY17	178	200	forward 3	TM	Transmembrane
292	U:2121610.13:2001MAY17	201	220	forward 3	TM	Cytosolic
292	U:2121610.13:2001MAY17	221	238	forward 3	TM	Transmembrane
292	U:2121610.13:2001MAY17	239	250	forward 3	TM	Non-Cytosolic
292	U:2121610.13:2001MAY17	251	269	forward 3	TM	Transmembrane
292	U:2121610.13:2001MAY17	270	316	forward 3	TM	Cytosolic
293	U:2191585.1:2001MAY17	1	72	forward 1	TM	Non-Cytosolic
293	U:2191585.1:2001MAY17	73	95	forward 1	TM	Transmembrane
293	U:2191585.1:2001MAY17	96	147	forward 1	TM	Cytosolic
293	U:2191585.1:2001MAY17	148	167	forward 1	TM	Transmembrane
293	U:2191585.1:2001MAY17	168	176	forward 1	TM	Non-Cytosolic
293	U:2191585.1:2001MAY17	177	199	forward 1	TM	Transmembrane
293	U:2191585.1:2001MAY17	200	239	forward 1	TM	Cytosolic
293	U:2191585.1:2001MAY17	240	262	forward 1	TM	Transmembrane
293	U:2191585.1:2001MAY17	263	298	forward 1	TM	Non-Cytosolic
294	U:2198562.3:2001MAY17	1	112	forward 2	TM	Cytosolic
294	U:2198562.3:2001MAY17	113	135	forward 2	TM	Transmembrane
294	U:2198562.3:2001MAY17	136	906	forward 2	TM	Non-Cytosolic
294	U:2198562.3:2001MAY17	1	117	forward 3	TM	Cytosolic
294	U:2198562.3:2001MAY17	118	140	forward 3	TM	Transmembrane
294	U:2198562.3:2001MAY17	141	905	forward 3	TM	Non-Cytosolic
295	U:2209684.5:2001MAY17	1	1501	forward 1	TM	Non-Cytosolic
295	U:2209684.5:2001MAY17	1502	1524	forward 1	TM	Transmembrane
295	U:2209684.5:2001MAY17	1525	1530	forward 1	TM	Cytosolic
295	U:2209684.5:2001MAY17	1531	1553	forward 1	TM	Transmembrane
295	U:2209684.5:2001MAY17	1554	1804	forward 1	TM	Non-Cytosolic
295	U:2209684.5:2001MAY17	1805	1827	forward 1	TM	Transmembrane
295	U:2209684.5:2001MAY17	1828	1840	forward 1	TM	Cytosolic
295	U:2209684.5:2001MAY17	1	837	forward 2	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
295	U:2209684.5:2001MAY17	838	860	forward 2	TM	Transmembrane
295	U:2209684.5:2001MAY17	861	971	forward 2	TM	Cytosolic
295	U:2209684.5:2001MAY17	972	994	forward 2	TM	Transmembrane
295	U:2209684.5:2001MAY17	995	1033	forward 2	TM	Non-Cytosolic
295	U:2209684.5:2001MAY17	1034	1056	forward 2	TM	Transmembrane
295	U:2209684.5:2001MAY17	1057	1068	forward 2	TM	Cytosolic
295	U:2209684.5:2001MAY17	1069	1091	forward 2	TM	Transmembrane
295	U:2209684.5:2001MAY17	1092	1100	forward 2	TM	Non-Cytosolic
295	U:2209684.5:2001MAY17	1101	1123	forward 2	TM	Transmembrane
295	U:2209684.5:2001MAY17	1124	1527	forward 2	TM	Cytosolic
295	U:2209684.5:2001MAY17	1528	1550	forward 2	TM	Transmembrane
295	U:2209684.5:2001MAY17	1551	1601	forward 2	TM	Non-Cytosolic
295	U:2209684.5:2001MAY17	1602	1619	forward 2	TM	Transmembrane
295	U:2209684.5:2001MAY17	1620	1797	forward 2	TM	Cytosolic
295	U:2209684.5:2001MAY17	1798	1817	forward 2	TM	Transmembrane
295	U:2209684.5:2001MAY17	1818	1840	forward 2	TM	Non-Cytosolic
295	U:2209684.5:2001MAY17	1	837	forward 3	TM	Non-Cytosolic
295	U:2209684.5:2001MAY17	838	860	forward 3	TM	Transmembrane
295	U:2209684.5:2001MAY17	861	970	forward 3	TM	Cytosolic
295	U:2209684.5:2001MAY17	971	993	forward 3	TM	Transmembrane
295	U:2209684.5:2001MAY17	994	1084	forward 3	TM	Non-Cytosolic
295	U:2209684.5:2001MAY17	1085	1107	forward 3	TM	Transmembrane
295	U:2209684.5:2001MAY17	1108	1532	forward 3	TM	Cytosolic
295	U:2209684.5:2001MAY17	1533	1555	forward 3	TM	Transmembrane
295	U:2209684.5:2001MAY17	1556	1569	forward 3	TM	Non-Cytosolic
295	U:2209684.5:2001MAY17	1570	1589	forward 3	TM	Transmembrane
295	U:2209684.5:2001MAY17	1590	1600	forward 3	TM	Cytosolic
295	U:2209684.5:2001MAY17	1601	1623	forward 3	TM	Transmembrane
295	U:2209684.5:2001MAY17	1624	1839	forward 3	TM	Non-Cytosolic
296	U:222795.28:2001MAY17	1	1525	forward 1	TM	Non-Cytosolic
296	U:222795.28:2001MAY17	1526	1548	forward 1	TM	Transmembrane
296	U:222795.28:2001MAY17	1549	1686	forward 1	TM	Cytosolic
297	U:228273.25:2001MAY17	1	1378	forward 2	TM	Non-Cytosolic
297	U:228273.25:2001MAY17	1379	1401	forward 2	TM	Transmembrane
297	U:228273.25:2001MAY17	1402	1501	forward 2	TM	Cytosolic
297	U:228273.25:2001MAY17	1	45	forward 3	TM	Cytosolic
297	U:228273.25:2001MAY17	46	68	forward 3	TM	Transmembrane
297	U:228273.25:2001MAY17	69	659	forward 3	TM	Non-Cytosolic
297	U:228273.25:2001MAY17	660	682	forward 3	TM	Transmembrane
297	U:228273.25:2001MAY17	683	694	forward 3	TM	Cytosolic
297	U:228273.25:2001MAY17	695	717	forward 3	TM	Transmembrane
297	U:228273.25:2001MAY17	718	1501	forward 3	TM	Non-Cytosolic
298	U:232386.31:2001MAY17	1	1013	forward 1	TM	Non-Cytosolic
298	U:232386.31:2001MAY17	1014	1032	forward 1	TM	Transmembrane
298	U:232386.31:2001MAY17	1033	1074	forward 1	TM	Cytosolic
298	U:232386.31:2001MAY17	1075	1097	forward 1	TM	Transmembrane
298	U:232386.31:2001MAY17	1098	1153	forward 1	TM	Non-Cytosolic
298	U:232386.31:2001MAY17	1	1012	forward 2	TM	Non-Cytosolic
298	U:232386.31:2001MAY17	1013	1032	forward 2	TM	Transmembrane
298	U:232386.31:2001MAY17	1033	1089	forward 2	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
298	U:232386.31:2001MAY17	1090	1112	forward 2	TM	Transmembrane
298	U:232386.31:2001MAY17	1113	1126	forward 2	TM	Non-Cytosolic
298	U:232386.31:2001MAY17	1127	1149	forward 2	TM	Transmembrane
298	U:232386.31:2001MAY17	1150	1153	forward 2	TM	Cytosolic
298	U:232386.31:2001MAY17	1	714	forward 3	TM	Non-Cytosolic
298	U:232386.31:2001MAY17	715	737	forward 3	TM	Transmembrane
298	U:232386.31:2001MAY17	738	940	forward 3	TM	Cytosolic
298	U:232386.31:2001MAY17	941	958	forward 3	TM	Transmembrane
298	U:232386.31:2001MAY17	959	972	forward 3	TM	Non-Cytosolic
298	U:232386.31:2001MAY17	973	992	forward 3	TM	Transmembrane
298	U:232386.31:2001MAY17	993	1089	forward 3	TM	Cytosolic
298	U:232386.31:2001MAY17	1090	1112	forward 3	TM	Transmembrane
298	U:232386.31:2001MAY17	1113	1121	forward 3	TM	Non-Cytosolic
298	U:232386.31:2001MAY17	1122	1144	forward 3	TM	Transmembrane
298	U:232386.31:2001MAY17	1145	1153	forward 3	TM	Cytosolic
299	U:233089.2:2001MAY17	1	54	forward 1	TM	Cytosolic
299	U:233089.2:2001MAY17	55	77	forward 1	TM	Transmembrane
299	U:233089.2:2001MAY17	78	81	forward 1	TM	Non-Cytosolic
299	U:233089.2:2001MAY17	82	104	forward 1	TM	Transmembrane
299	U:233089.2:2001MAY17	105	116	forward 1	TM	Cytosolic
299	U:233089.2:2001MAY17	117	136	forward 1	TM	Transmembrane
299	U:233089.2:2001MAY17	137	1055	forward 1	TM	Non-Cytosolic
299	U:233089.2:2001MAY17	1056	1078	forward 1	TM	Transmembrane
299	U:233089.2:2001MAY17	1079	1090	forward 1	TM	Cytosolic
299	U:233089.2:2001MAY17	1091	1113	forward 1	TM	Transmembrane
299	U:233089.2:2001MAY17	1114	1151	forward 1	TM	Non-Cytosolic
299	U:233089.2:2001MAY17	1152	1174	forward 1	TM	Transmembrane
299	U:233089.2:2001MAY17	1175	1279	forward 1	TM	Cytosolic
299	U:233089.2:2001MAY17	1280	1297	forward 1	TM	Transmembrane
299	U:233089.2:2001MAY17	1298	1316	forward 1	TM	Non-Cytosolic
299	U:233089.2:2001MAY17	1317	1339	forward 1	TM	Transmembrane
299	U:233089.2:2001MAY17	1340	1357	forward 1	TM	Cytosolic
299	U:233089.2:2001MAY17	1358	1380	forward 1	TM	Transmembrane
299	U:233089.2:2001MAY17	1381	1954	forward 1	TM	Non-Cytosolic
299	U:233089.2:2001MAY17	1	1069	forward 2	TM	Non-Cytosolic
299	U:233089.2:2001MAY17	1070	1087	forward 2	TM	Transmembrane
299	U:233089.2:2001MAY17	1088	1106	forward 2	TM	Cytosolic
299	U:233089.2:2001MAY17	1107	1129	forward 2	TM	Transmembrane
299	U:233089.2:2001MAY17	1130	1551	forward 2	TM	Non-Cytosolic
299	U:233089.2:2001MAY17	1552	1574	forward 2	TM	Transmembrane
299	U:233089.2:2001MAY17	1575	1857	forward 2	TM	Cytosolic
299	U:233089.2:2001MAY17	1858	1880	forward 2	TM	Transmembrane
299	U:233089.2:2001MAY17	1881	1884	forward 2	TM	Non-Cytosolic
299	U:233089.2:2001MAY17	1885	1907	forward 2	TM	Transmembrane
299	U:233089.2:2001MAY17	1908	1954	forward 2	TM	Cytosolic
299	U:233089.2:2001MAY17	1	987	forward 3	TM	Non-Cytosolic
299	U:233089.2:2001MAY17	988	1010	forward 3	TM	Transmembrane
299	U:233089.2:2001MAY17	1011	1124	forward 3	TM	Cytosolic
299	U:233089.2:2001MAY17	1125	1147	forward 3	TM	Transmembrane
299	U:233089.2:2001MAY17	1148	1161	forward 3	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
299	U:233089.2:2001MAY17	1162	1184	forward 3	TM	Transmembrane
299	U:233089.2:2001MAY17	1185	1216	forward 3	TM	Cytosolic
299	U:233089.2:2001MAY17	1217	1234	forward 3	TM	Transmembrane
299	U:233089.2:2001MAY17	1235	1458	forward 3	TM	Non-Cytosolic
299	U:233089.2:2001MAY17	1459	1481	forward 3	TM	Transmembrane
299	U:233089.2:2001MAY17	1482	1549	forward 3	TM	Cytosolic
299	U:233089.2:2001MAY17	1550	1572	forward 3	TM	Transmembrane
299	U:233089.2:2001MAY17	1573	1954	forward 3	TM	Non-Cytosolic
300	U:240641.10:2001MAY17	1	608	forward 1	TM	Non-Cytosolic
300	U:240641.10:2001MAY17	609	631	forward 1	TM	Transmembrane
300	U:240641.10:2001MAY17	632	650	forward 1	TM	Cytosolic
300	U:240641.10:2001MAY17	651	670	forward 1	TM	Transmembrane
300	U:240641.10:2001MAY17	671	1345	forward 1	TM	Non-Cytosolic
301	U:243871.4:2001MAY17	1	361	forward 1	TM	Non-Cytosolic
301	U:243871.4:2001MAY17	362	384	forward 1	TM	Transmembrane
301	U:243871.4:2001MAY17	385	390	forward 1	TM	Cytosolic
301	U:243871.4:2001MAY17	391	413	forward 1	TM	Transmembrane
301	U:243871.4:2001MAY17	414	682	forward 1	TM	Non-Cytosolic
301	U:243871.4:2001MAY17	1	365	forward 2	TM	Non-Cytosolic
301	U:243871.4:2001MAY17	366	385	forward 2	TM	Transmembrane
301	U:243871.4:2001MAY17	386	391	forward 2	TM	Cytosolic
301	U:243871.4:2001MAY17	392	414	forward 2	TM	Transmembrane
301	U:243871.4:2001MAY17	415	464	forward 2	TM	Non-Cytosolic
301	U:243871.4:2001MAY17	465	487	forward 2	TM	Transmembrane
301	U:243871.4:2001MAY17	488	662	forward 2	TM	Cytosolic
301	U:243871.4:2001MAY17	663	681	forward 2	TM	Transmembrane
301	U:243871.4:2001MAY17	682	682	forward 2	TM	Non-Cytosolic
302	U:245597.7:2001MAY17	1	1382	forward 1	TM	Non-Cytosolic
302	U:245597.7:2001MAY17	1383	1405	forward 1	TM	Transmembrane
302	U:245597.7:2001MAY17	1406	1415	forward 1	TM	Cytosolic
302	U:245597.7:2001MAY17	1	1224	forward 2	TM	Non-Cytosolic
302	U:245597.7:2001MAY17	1225	1247	forward 2	TM	Transmembrane
302	U:245597.7:2001MAY17	1248	1267	forward 2	TM	Cytosolic
302	U:245597.7:2001MAY17	1268	1290	forward 2	TM	Transmembrane
302	U:245597.7:2001MAY17	1291	1304	forward 2	TM	Non-Cytosolic
302	U:245597.7:2001MAY17	1305	1324	forward 2	TM	Transmembrane
302	U:245597.7:2001MAY17	1325	1366	forward 2	TM	Cytosolic
302	U:245597.7:2001MAY17	1367	1386	forward 2	TM	Transmembrane
302	U:245597.7:2001MAY17	1387	1389	forward 2	TM	Non-Cytosolic
302	U:245597.7:2001MAY17	1390	1407	forward 2	TM	Transmembrane
302	U:245597.7:2001MAY17	1408	1415	forward 2	TM	Cytosolic
302	U:245597.7:2001MAY17	1	34	forward 3	TM	Cytosolic
302	U:245597.7:2001MAY17	35	57	forward 3	TM	Transmembrane
302	U:245597.7:2001MAY17	58	957	forward 3	TM	Non-Cytosolic
302	U:245597.7:2001MAY17	958	980	forward 3	TM	Transmembrane
302	U:245597.7:2001MAY17	981	1199	forward 3	TM	Cytosolic
302	U:245597.7:2001MAY17	1200	1222	forward 3	TM	Transmembrane
302	U:245597.7:2001MAY17	1223	1305	forward 3	TM	Non-Cytosolic
302	U:245597.7:2001MAY17	1306	1328	forward 3	TM	Transmembrane
302	U:245597.7:2001MAY17	1329	1369	forward 3	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
302	U:245597.7:2001MAY17	1370	1392	forward 3	TM	Transmembrane
302	U:245597.7:2001MAY17	1393	1415	forward 3	TM	Non-Cytosolic
303	U:256009.31:2001MAY17	1	53	forward 3	TM	Non-Cytosolic
303	U:256009.31:2001MAY17	54	76	forward 3	TM	Transmembrane
303	U:256009.31:2001MAY17	77	250	forward 3	TM	Cytosolic
303	U:256009.31:2001MAY17	251	273	forward 3	TM	Transmembrane
303	U:256009.31:2001MAY17	274	314	forward 3	TM	Non-Cytosolic
303	U:256009.31:2001MAY17	315	334	forward 3	TM	Transmembrane
303	U:256009.31:2001MAY17	335	499	forward 3	TM	Cytosolic
304	U:262221.1:2001MAY17	1	148	forward 1	TM	Cytosolic
304	U:262221.1:2001MAY17	149	171	forward 1	TM	Transmembrane
304	U:262221.1:2001MAY17	172	732	forward 1	TM	Non-Cytosolic
305	U:332957.8:2001MAY17	1	300	forward 1	TM	Non-Cytosolic
305	U:332957.8:2001MAY17	301	323	forward 1	TM	Transmembrane
305	U:332957.8:2001MAY17	324	537	forward 1	TM	Cytosolic
305	U:332957.8:2001MAY17	538	560	forward 1	TM	Transmembrane
305	U:332957.8:2001MAY17	561	1491	forward 1	TM	Non-Cytosolic
305	U:332957.8:2001MAY17	1	435	forward 3	TM	Non-Cytosolic
305	U:332957.8:2001MAY17	436	455	forward 3	TM	Transmembrane
305	U:332957.8:2001MAY17	456	535	forward 3	TM	Cytosolic
305	U:332957.8:2001MAY17	536	558	forward 3	TM	Transmembrane
305	U:332957.8:2001MAY17	559	1027	forward 3	TM	Non-Cytosolic
305	U:332957.8:2001MAY17	1028	1050	forward 3	TM	Transmembrane
305	U:332957.8:2001MAY17	1051	1062	forward 3	TM	Cytosolic
305	U:332957.8:2001MAY17	1063	1085	forward 3	TM	Transmembrane
305	U:332957.8:2001MAY17	1086	1490	forward 3	TM	Non-Cytosolic
306	U:335352.13:2001MAY17	1	144	forward 1	TM	Non-Cytosolic
306	U:335352.13:2001MAY17	145	167	forward 1	TM	Transmembrane
306	U:335352.13:2001MAY17	168	330	forward 1	TM	Cytosolic
306	U:335352.13:2001MAY17	331	353	forward 1	TM	Transmembrane
306	U:335352.13:2001MAY17	354	425	forward 1	TM	Non-Cytosolic
306	U:335352.13:2001MAY17	426	448	forward 1	TM	Transmembrane
306	U:335352.13:2001MAY17	449	460	forward 1	TM	Cytosolic
306	U:335352.13:2001MAY17	461	483	forward 1	TM	Transmembrane
306	U:335352.13:2001MAY17	484	492	forward 1	TM	Non-Cytosolic
306	U:335352.13:2001MAY17	493	510	forward 1	TM	Transmembrane
306	U:335352.13:2001MAY17	511	553	forward 1	TM	Cytosolic
306	U:335352.13:2001MAY17	554	576	forward 1	TM	Transmembrane
306	U:335352.13:2001MAY17	577	616	forward 1	TM	Non-Cytosolic
306	U:335352.13:2001MAY17	617	639	forward 1	TM	Transmembrane
306	U:335352.13:2001MAY17	640	645	forward 1	TM	Cytosolic
306	U:335352.13:2001MAY17	646	668	forward 1	TM	Transmembrane
306	U:335352.13:2001MAY17	669	766	forward 1	TM	Non-Cytosolic
306	U:335352.13:2001MAY17	767	789	forward 1	TM	Transmembrane
306	U:335352.13:2001MAY17	790	905	forward 1	TM	Cytosolic
306	U:335352.13:2001MAY17	906	928	forward 1	TM	Transmembrane
306	U:335352.13:2001MAY17	929	970	forward 1	TM	Non-Cytosolic
306	U:335352.13:2001MAY17	971	993	forward 1	TM	Transmembrane
306	U:335352.13:2001MAY17	994	1046	forward 1	TM	Cytosolic
306	U:335352.13:2001MAY17	1047	1069	forward 1	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
306	U:335352.13:2001MAY17	1070	1072	forward 1	TM	Non-Cytosolic
306	U:335352.13:2001MAY17	1073	1091	forward 1	TM	Transmembrane
306	U:335352.13:2001MAY17	1092	1096	forward 1	TM	Cytosolic
306	U:335352.13:2001MAY17	1	427	forward 2	TM	Non-Cytosolic
306	U:335352.13:2001MAY17	428	450	forward 2	TM	Transmembrane
306	U:335352.13:2001MAY17	451	496	forward 2	TM	Cytosolic
306	U:335352.13:2001MAY17	497	516	forward 2	TM	Transmembrane
306	U:335352.13:2001MAY17	517	519	forward 2	TM	Non-Cytosolic
306	U:335352.13:2001MAY17	520	539	forward 2	TM	Transmembrane
306	U:335352.13:2001MAY17	540	551	forward 2	TM	Cytosolic
306	U:335352.13:2001MAY17	552	574	forward 2	TM	Transmembrane
306	U:335352.13:2001MAY17	575	657	forward 2	TM	Non-Cytosolic
306	U:335352.13:2001MAY17	658	680	forward 2	TM	Transmembrane
306	U:335352.13:2001MAY17	681	699	forward 2	TM	Cytosolic
306	U:335352.13:2001MAY17	700	719	forward 2	TM	Transmembrane
306	U:335352.13:2001MAY17	720	1096	forward 2	TM	Non-Cytosolic
306	U:335352.13:2001MAY17	1	135	forward 3	TM	Cytosolic
306	U:335352.13:2001MAY17	136	158	forward 3	TM	Transmembrane
306	U:335352.13:2001MAY17	159	197	forward 3	TM	Non-Cytosolic
306	U:335352.13:2001MAY17	198	220	forward 3	TM	Transmembrane
306	U:335352.13:2001MAY17	221	329	forward 3	TM	Cytosolic
306	U:335352.13:2001MAY17	330	352	forward 3	TM	Transmembrane
306	U:335352.13:2001MAY17	353	454	forward 3	TM	Non-Cytosolic
306	U:335352.13:2001MAY17	455	477	forward 3	TM	Transmembrane
306	U:335352.13:2001MAY17	478	497	forward 3	TM	Cytosolic
306	U:335352.13:2001MAY17	498	520	forward 3	TM	Transmembrane
306	U:335352.13:2001MAY17	521	551	forward 3	TM	Non-Cytosolic
306	U:335352.13:2001MAY17	552	574	forward 3	TM	Transmembrane
306	U:335352.13:2001MAY17	575	593	forward 3	TM	Cytosolic
306	U:335352.13:2001MAY17	594	616	forward 3	TM	Transmembrane
306	U:335352.13:2001MAY17	617	635	forward 3	TM	Non-Cytosolic
306	U:335352.13:2001MAY17	636	658	forward 3	TM	Transmembrane
306	U:335352.13:2001MAY17	659	919	forward 3	TM	Cytosolic
306	U:335352.13:2001MAY17	920	942	forward 3	TM	Transmembrane
306	U:335352.13:2001MAY17	943	956	forward 3	TM	Non-Cytosolic
306	U:335352.13:2001MAY17	957	979	forward 3	TM	Transmembrane
306	U:335352.13:2001MAY17	980	1017	forward 3	TM	Cytosolic
306	U:335352.13:2001MAY17	1018	1035	forward 3	TM	Transmembrane
306	U:335352.13:2001MAY17	1036	1044	forward 3	TM	Non-Cytosolic
306	U:335352.13:2001MAY17	1045	1067	forward 3	TM	Transmembrane
306	U:335352.13:2001MAY17	1068	1073	forward 3	TM	Cytosolic
306	U:335352.13:2001MAY17	1074	1092	forward 3	TM	Transmembrane
306	U:335352.13:2001MAY17	1093	1095	forward 3	TM	Non-Cytosolic
307	U:343844.7:2001MAY17	1	343	forward 2	TM	Non-Cytosolic
307	U:343844.7:2001MAY17	344	366	forward 2	TM	Transmembrane
307	U:343844.7:2001MAY17	367	377	forward 2	TM	Cytosolic
307	U:343844.7:2001MAY17	378	400	forward 2	TM	Transmembrane
307	U:343844.7:2001MAY17	401	404	forward 2	TM	Non-Cytosolic
307	U:343844.7:2001MAY17	405	422	forward 2	TM	Transmembrane
307	U:343844.7:2001MAY17	423	426	forward 2	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
308	U:344528.1:2001MAY17	1	940	forward 1	TM	Non-Cytosolic
308	U:344528.1:2001MAY17	941	963	forward 1	TM	Transmembrane
308	U:344528.1:2001MAY17	964	1309	forward 1	TM	Cytosolic
308	U:344528.1:2001MAY17	1310	1332	forward 1	TM	Transmembrane
308	U:344528.1:2001MAY17	1333	1349	forward 1	TM	Non-Cytosolic
308	U:344528.1:2001MAY17	1	853	forward 2	TM	Non-Cytosolic
308	U:344528.1:2001MAY17	854	876	forward 2	TM	Transmembrane
308	U:344528.1:2001MAY17	877	929	forward 2	TM	Cytosolic
308	U:344528.1:2001MAY17	930	952	forward 2	TM	Transmembrane
308	U:344528.1:2001MAY17	953	1349	forward 2	TM	Non-Cytosolic
309	U:374578.27:2001MAY17	1	496	forward 1	TM	Cytosolic
309	U:374578.27:2001MAY17	497	519	forward 1	TM	Transmembrane
309	U:374578.27:2001MAY17	520	523	forward 1	TM	Non-Cytosolic
309	U:374578.27:2001MAY17	1	496	forward 2	TM	Non-Cytosolic
309	U:374578.27:2001MAY17	497	519	forward 2	TM	Transmembrane
309	U:374578.27:2001MAY17	520	523	forward 2	TM	Cytosolic
309	U:374578.27:2001MAY17	1	495	forward 3	TM	Non-Cytosolic
309	U:374578.27:2001MAY17	496	518	forward 3	TM	Transmembrane
309	U:374578.27:2001MAY17	519	523	forward 3	TM	Cytosolic
310	U:381993.13:2001MAY17	1	69	forward 1	TM	Cytosolic
310	U:381993.13:2001MAY17	70	89	forward 1	TM	Transmembrane
310	U:381993.13:2001MAY17	90	103	forward 1	TM	Non-Cytosolic
310	U:381993.13:2001MAY17	104	126	forward 1	TM	Transmembrane
310	U:381993.13:2001MAY17	127	138	forward 1	TM	Cytosolic
310	U:381993.13:2001MAY17	139	161	forward 1	TM	Transmembrane
310	U:381993.13:2001MAY17	162	205	forward 1	TM	Non-Cytosolic
310	U:381993.13:2001MAY17	206	225	forward 1	TM	Transmembrane
310	U:381993.13:2001MAY17	226	394	forward 1	TM	Cytosolic
310	U:381993.13:2001MAY17	395	417	forward 1	TM	Transmembrane
310	U:381993.13:2001MAY17	418	2098	forward 1	TM	Non-Cytosolic
310	U:381993.13:2001MAY17	2099	2121	forward 1	TM	Transmembrane
310	U:381993.13:2001MAY17	2122	2239	forward 1	TM	Cytosolic
310	U:381993.13:2001MAY17	2240	2262	forward 1	TM	Transmembrane
310	U:381993.13:2001MAY17	2263	2282	forward 1	TM	Non-Cytosolic
310	U:381993.13:2001MAY17	1	150	forward 2	TM	Cytosolic
310	U:381993.13:2001MAY17	151	173	forward 2	TM	Transmembrane
310	U:381993.13:2001MAY17	174	177	forward 2	TM	Non-Cytosolic
310	U:381993.13:2001MAY17	178	195	forward 2	TM	Transmembrane
310	U:381993.13:2001MAY17	196	201	forward 2	TM	Cytosolic
310	U:381993.13:2001MAY17	202	224	forward 2	TM	Transmembrane
310	U:381993.13:2001MAY17	225	1670	forward 2	TM	Non-Cytosolic
310	U:381993.13:2001MAY17	1671	1693	forward 2	TM	Transmembrane
310	U:381993.13:2001MAY17	1694	2196	forward 2	TM	Cytosolic
310	U:381993.13:2001MAY17	2197	2216	forward 2	TM	Transmembrane
310	U:381993.13:2001MAY17	2217	2239	forward 2	TM	Non-Cytosolic
310	U:381993.13:2001MAY17	2240	2262	forward 2	TM	Transmembrane
310	U:381993.13:2001MAY17	2263	2282	forward 2	TM	Cytosolic
310	U:381993.13:2001MAY17	1	20	forward 3	TM	Cytosolic
310	U:381993.13:2001MAY17	21	43	forward 3	TM	Transmembrane
310	U:381993.13:2001MAY17	44	102	forward 3	TM	Non-Cytosolic



TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
310	U:381993.13:2001MAY17	103	125	forward 3	TM	Transmembrane
310	U:381993.13:2001MAY17	126	144	forward 3	TM	Cytosolic
310	U:381993.13:2001MAY17	145	167	forward 3	TM	Transmembrane
310	U:381993.13:2001MAY17	168	1179	forward 3	TM	Non-Cytosolic
310	U:381993.13:2001MAY17	1180	1202	forward 3	TM	Transmembrane
310	U:381993.13:2001MAY17	1203	1342	forward 3	TM	Cytosolic
310	U:381993.13:2001MAY17	1343	1362	forward 3	TM	Transmembrane
310	U:381993.13:2001MAY17	1363	1381	forward 3	TM	Non-Cytosolic
310	U:381993.13:2001MAY17	1382	1401	forward 3	TM	Transmembrane
310	U:381993.13:2001MAY17	1402	1421	forward 3	TM	Cytosolic
310	U:381993.13:2001MAY17	1422	1444	forward 3	TM	Transmembrane
310	U:381993.13:2001MAY17	1445	1453	forward 3	TM	Non-Cytosolic
310	U:381993.13:2001MAY17	1454	1471	forward 3	TM	Transmembrane
310	U:381993.13:2001MAY17	1472	1477	forward 3	TM	Cytosolic
310	U:381993.13:2001MAY17	1478	1500	forward 3	TM	Transmembrane
310	U:381993.13:2001MAY17	1501	2282	forward 3	TM	Non-Cytosolic
311	U:400373.2:2001MAY17	1	145	forward 1	TM	Non-Cytosolic
311	U:400373.2:2001MAY17	146	168	forward 1	TM	Transmembrane
311	U:400373.2:2001MAY17	169	469	forward 1	TM	Cytosolic
311	U:400373.2:2001MAY17	470	492	forward 1	TM	Transmembrane
311	U:400373.2:2001MAY17	493	1295	forward 1	TM	Non-Cytosolic
311	U:400373.2:2001MAY17	1	1245	forward 2	TM	Non-Cytosolic
311	U:400373.2:2001MAY17	1246	1268	forward 2	TM	Transmembrane
311	U:400373.2:2001MAY17	1269	1295	forward 2	TM	Cytosolic
311	U:400373.2:2001MAY17	1	850	forward 3	TM	Non-Cytosolic
311	U:400373.2:2001MAY17	851	873	forward 3	TM	Transmembrane
311	U:400373.2:2001MAY17	874	1049	forward 3	TM	Cytosolic
311	U:400373.2:2001MAY17	1050	1072	forward 3	TM	Transmembrane
311	U:400373.2:2001MAY17	1073	1231	forward 3	TM	Non-Cytosolic
311	U:400373.2:2001MAY17	1232	1254	forward 3	TM	Transmembrane
311	U:400373.2:2001MAY17	1255	1258	forward 3	TM	Cytosolic
311	U:400373.2:2001MAY17	1259	1281	forward 3	TM	Transmembrane
311	U:400373.2:2001MAY17	1282	1295	forward 3	TM	Non-Cytosolic
312	U:400963.6:2001MAY17	1	1292	forward 2	TM	Non-Cytosolic
312	U:400963.6:2001MAY17	1293	1315	forward 2	TM	Transmembrane
312	U:400963.6:2001MAY17	1316	1318	forward 2	TM	Cytosolic
313	U:404874.8:2001MAY17	1	1121	forward 2	TM	Non-Cytosolic
313	U:404874.8:2001MAY17	1122	1144	forward 2	TM	Transmembrane
313	U:404874.8:2001MAY17	1145	1150	forward 2	TM	Cytosolic
313	U:404874.8:2001MAY17	1151	1173	forward 2	TM	Transmembrane
313	U:404874.8:2001MAY17	1174	1200	forward 2	TM	Non-Cytosolic
313	U:404874.8:2001MAY17	1201	1223	forward 2	TM	Transmembrane
313	U:404874.8:2001MAY17	1224	1245	forward 2	TM	Cytosolic
313	U:404874.8:2001MAY17	1	1029	forward 3	TM	Non-Cytosolic
313	U:404874.8:2001MAY17	1030	1052	forward 3	TM	Transmembrane
313	U:404874.8:2001MAY17	1053	1123	forward 3	TM	Cytosolic
313	U:404874.8:2001MAY17	1124	1146	forward 3	TM	Transmembrane
313	U:404874.8:2001MAY17	1147	1190	forward 3	TM	Non-Cytosolic
313	U:404874.8:2001MAY17	1191	1213	forward 3	TM	Transmembrane
313	U:404874.8:2001MAY17	1214	1244	forward 3	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
314	U:405158.18:2001MAY17	1	1358	forward 1	TM	Non-Cytosolic
314	U:405158.18:2001MAY17	1359	1381	forward 1	TM	Transmembrane
314	U:405158.18:2001MAY17	1382	1470	forward 1	TM	Cytosolic
314	U:405158.18:2001MAY17	1471	1493	forward 1	TM	Transmembrane
314	U:405158.18:2001MAY17	1494	1518	forward 1	TM	Non-Cytosolic
314	U:405158.18:2001MAY17	1519	1541	forward 1	TM	Transmembrane
314	U:405158.18:2001MAY17	1542	1629	forward 1	TM	Cytosolic
314	U:405158.18:2001MAY17	1630	1652	forward 1	TM	Transmembrane
314	U:405158.18:2001MAY17	1653	1753	forward 1	TM	Non-Cytosolic
314	U:405158.18:2001MAY17	1754	1776	forward 1	TM	Transmembrane
314	U:405158.18:2001MAY17	1777	1847	forward 1	TM	Cytosolic
314	U:405158.18:2001MAY17	1848	1870	forward 1	TM	Transmembrane
314	U:405158.18:2001MAY17	1871	1974	forward 1	TM	Non-Cytosolic
314	U:405158.18:2001MAY17	1975	1997	forward 1	TM	Transmembrane
314	U:405158.18:2001MAY17	1998	2009	forward 1	TM	Cytosolic
314	U:405158.18:2001MAY17	2010	2032	forward 1	TM	Transmembrane
314	U:405158.18:2001MAY17	2033	2059	forward 1	TM	Non-Cytosolic
314	U:405158.18:2001MAY17	2060	2082	forward 1	TM	Transmembrane
314	U:405158.18:2001MAY17	2083	2248	forward 1	TM	Cytosolic
314	U:405158.18:2001MAY17	1	1266	forward 2	TM	Non-Cytosolic
314	U:405158.18:2001MAY17	1267	1289	forward 2	TM	Transmembrane
314	U:405158.18:2001MAY17	1290	1510	forward 2	TM	Cytosolic
314	U:405158.18:2001MAY17	1511	1533	forward 2	TM	Transmembrane
314	U:405158.18:2001MAY17	1534	1757	forward 2	TM	Non-Cytosolic
314	U:405158.18:2001MAY17	1758	1780	forward 2	TM	Transmembrane
314	U:405158.18:2001MAY17	1781	1786	forward 2	TM	Cytosolic
314	U:405158.18:2001MAY17	1787	1809	forward 2	TM	Transmembrane
314	U:405158.18:2001MAY17	1810	1823	forward 2	TM	Non-Cytosolic
314	U:405158.18:2001MAY17	1824	1846	forward 2	TM	Transmembrane
314	U:405158.18:2001MAY17	1847	1914	forward 2	TM	Cytosolic
314	U:405158.18:2001MAY17	1915	1937	forward 2	TM	Transmembrane
314	U:405158.18:2001MAY17	1938	1975	forward 2	TM	Non-Cytosolic
314	U:405158.18:2001MAY17	1976	1998	forward 2	TM	Transmembrane
314	U:405158.18:2001MAY17	1999	2017	forward 2	TM	Cytosolic
314	U:405158.18:2001MAY17	2018	2040	forward 2	TM	Transmembrane
314	U:405158.18:2001MAY17	2041	2059	forward 2	TM	Non-Cytosolic
314	U:405158.18:2001MAY17	2060	2082	forward 2	TM	Transmembrane
314	U:405158.18:2001MAY17	2083	2144	forward 2	TM	Cytosolic
314	U:405158.18:2001MAY17	2145	2167	forward 2	TM	Transmembrane
314	U:405158.18:2001MAY17	2168	2181	forward 2	TM	Non-Cytosolic
314	U:405158.18:2001MAY17	2182	2204	forward 2	TM	Transmembrane
314	U:405158.18:2001MAY17	2205	2224	forward 2	TM	Cytosolic
314	U:405158.18:2001MAY17	2225	2247	forward 2	TM	Transmembrane
314	U:405158.18:2001MAY17	2248	2248	forward 2	TM	Non-Cytosolic
314	U:405158.18:2001MAY17	1	445	forward 3	TM	Non-Cytosolic
314	U:405158.18:2001MAY17	446	468	forward 3	TM	Transmembrane
314	U:405158.18:2001MAY17	469	497	forward 3	TM	Cytosolic
314	U:405158.18:2001MAY17	498	515	forward 3	TM	Transmembrane
314	U:405158.18:2001MAY17	516	1821	forward 3	TM	Non-Cytosolic
314	U:405158.18:2001MAY17	1822	1844	forward 3	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
314	U:405158.18:2001MAY17	1845	1902	forward 3	TM	Cytosolic
314	U:405158.18:2001MAY17	1903	1925	forward 3	TM	Transmembrane
314	U:405158.18:2001MAY17	1926	1944	forward 3	TM	Non-Cytosolic
314	U:405158.18:2001MAY17	1945	1967	forward 3	TM	Transmembrane
314	U:405158.18:2001MAY17	1968	1979	forward 3	TM	Cytosolic
314	U:405158.18:2001MAY17	1980	1998	forward 3	TM	Transmembrane
314	U:405158.18:2001MAY17	1999	2017	forward 3	TM	Non-Cytosolic
314	U:405158.18:2001MAY17	2018	2040	forward 3	TM	Transmembrane
314	U:405158.18:2001MAY17	2041	2060	forward 3	TM	Cytosolic
314	U:405158.18:2001MAY17	2061	2083	forward 3	TM	Transmembrane
314	U:405158.18:2001MAY17	2084	2097	forward 3	TM	Non-Cytosolic
314	U:405158.18:2001MAY17	2098	2120	forward 3	TM	Transmembrane
314	U:405158.18:2001MAY17	2121	2149	forward 3	TM	Cytosolic
314	U:405158.18:2001MAY17	2150	2167	forward 3	TM	Transmembrane
314	U:405158.18:2001MAY17	2168	2208	forward 3	TM	Non-Cytosolic
314	U:405158.18:2001MAY17	2209	2231	forward 3	TM	Transmembrane
314	U:405158.18:2001MAY17	2232	2247	forward 3	TM	Cytosolic
315	U:405889.22:2001MAY17	1	172	forward 3	TM	Non-Cytosolic
315	U:405889.22:2001MAY17	173	195	forward 3	TM	Transmembrane
315	U:405889.22:2001MAY17	196	409	forward 3	TM	Cytosolic
315	U:405889.22:2001MAY17	410	432	forward 3	TM	Transmembrane
315	U:405889.22:2001MAY17	433	707	forward 3	TM	Non-Cytosolic
316	U:411151.31:2001MAY17	1	1126	forward 2	TM	Non-Cytosolic
316	U:411151.31:2001MAY17	1127	1149	forward 2	TM	Transmembrane
316	U:411151.31:2001MAY17	1150	1160	forward 2	TM	Cytosolic
316	U:411151.31:2001MAY17	1161	1183	forward 2	TM	Transmembrane
316	U:411151.31:2001MAY17	1184	1197	forward 2	TM	Non-Cytosolic
316	U:411151.31:2001MAY17	1198	1220	forward 2	TM	Transmembrane
316	U:411151.31:2001MAY17	1221	1239	forward 2	TM	Cytosolic
316	U:411151.31:2001MAY17	1240	1262	forward 2	TM	Transmembrane
316	U:411151.31:2001MAY17	1263	1481	forward 2	TM	Non-Cytosolic
317	U:411313.51:2001MAY17	1	1039	forward 3	TM	Non-Cytosolic
317	U:411313.51:2001MAY17	1040	1062	forward 3	TM	Transmembrane
317	U:411313.51:2001MAY17	1063	1085	forward 3	TM	Cytosolic
317	U:411313.51:2001MAY17	1086	1108	forward 3	TM	Transmembrane
317	U:411313.51:2001MAY17	1109	1152	forward 3	TM	Non-Cytosolic
318	U:417127.1:2001MAY17	1	44	forward 2	TM	Non-Cytosolic
318	U:417127.1:2001MAY17	45	67	forward 2	TM	Transmembrane
318	U:417127.1:2001MAY17	68	210	forward 2	TM	Cytosolic
319	U:429817.44:2001MAY17	1	407	forward 1	TM	Non-Cytosolic
319	U:429817.44:2001MAY17	408	430	forward 1	TM	Transmembrane
319	U:429817.44:2001MAY17	431	442	forward 1	TM	Cytosolic
319	U:429817.44:2001MAY17	443	465	forward 1	TM	Transmembrane
319	U:429817.44:2001MAY17	466	474	forward 1	TM	Non-Cytosolic
319	U:429817.44:2001MAY17	475	492	forward 1	TM	Transmembrane
319	U:429817.44:2001MAY17	493	574	forward 1	TM	Cytosolic
319	U:429817.44:2001MAY17	575	597	forward 1	TM	Transmembrane
319	U:429817.44:2001MAY17	598	611	forward 1	TM	Non-Cytosolic
319	U:429817.44:2001MAY17	612	634	forward 1	TM	Transmembrane
319	U:429817.44:2001MAY17	635	655	forward 1	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
319	U:429817.44:2001MAY17	1	262	forward 2	TM	Cytosolic
319	U:429817.44:2001MAY17	263	285	forward 2	TM	Transmembrane
319	U:429817.44:2001MAY17	286	361	forward 2	TM	Non-Cytosolic
319	U:429817.44:2001MAY17	362	384	forward 2	TM	Transmembrane
319	U:429817.44:2001MAY17	385	390	forward 2	TM	Cytosolic
319	U:429817.44:2001MAY17	391	413	forward 2	TM	Transmembrane
319	U:429817.44:2001MAY17	414	422	forward 2	TM	Non-Cytosolic
319	U:429817.44:2001MAY17	423	445	forward 2	TM	Transmembrane
319	U:429817.44:2001MAY17	446	583	forward 2	TM	Cytosolic
319	U:429817.44:2001MAY17	584	603	forward 2	TM	Transmembrane
319	U:429817.44:2001MAY17	604	612	forward 2	TM	Non-Cytosolic
319	U:429817.44:2001MAY17	613	635	forward 2	TM	Transmembrane
319	U:429817.44:2001MAY17	636	654	forward 2	TM	Cytosolic
319	U:429817.44:2001MAY17	1	262	forward 3	TM	Non-Cytosolic
319	U:429817.44:2001MAY17	263	285	forward 3	TM	Transmembrane
319	U:429817.44:2001MAY17	286	410	forward 3	TM	Cytosolic
319	U:429817.44:2001MAY17	411	433	forward 3	TM	Transmembrane
319	U:429817.44:2001MAY17	434	442	forward 3	TM	Non-Cytosolic
319	U:429817.44:2001MAY17	443	465	forward 3	TM	Transmembrane
319	U:429817.44:2001MAY17	466	566	forward 3	TM	Cytosolic
319	U:429817.44:2001MAY17	567	589	forward 3	TM	Transmembrane
319	U:429817.44:2001MAY17	590	610	forward 3	TM	Non-Cytosolic
319	U:429817.44:2001MAY17	611	633	forward 3	TM	Transmembrane
319	U:429817.44:2001MAY17	634	654	forward 3	TM	Cytosolic
320	U:474134.23:2001MAY17	1	329	forward 3	TM	Non-Cytosolic
320	U:474134.23:2001MAY17	330	352	forward 3	TM	Transmembrane
320	U:474134.23:2001MAY17	353	364	forward 3	TM	Cytosolic
320	U:474134.23:2001MAY17	365	382	forward 3	TM	Transmembrane
320	U:474134.23:2001MAY17	383	647	forward 3	TM	Non-Cytosolic
321	U:475378.3:2001MAY17	1	1181	forward 3	TM	Non-Cytosolic
321	U:475378.3:2001MAY17	1182	1204	forward 3	TM	Transmembrane
321	U:475378.3:2001MAY17	1205	1393	forward 3	TM	Cytosolic
321	U:475378.3:2001MAY17	1394	1416	forward 3	TM	Transmembrane
321	U:475378.3:2001MAY17	1417	1430	forward 3	TM	Non-Cytosolic
321	U:475378.3:2001MAY17	1431	1453	forward 3	TM	Transmembrane
321	U:475378.3:2001MAY17	1454	1473	forward 3	TM	Cytosolic
321	U:475378.3:2001MAY17	1474	1496	forward 3	TM	Transmembrane
321	U:475378.3:2001MAY17	1497	1541	forward 3	TM	Non-Cytosolic
321	U:475378.3:2001MAY17	1542	1564	forward 3	TM	Transmembrane
321	U:475378.3:2001MAY17	1565	1576	forward 3	TM	Cytosolic
321	U:475378.3:2001MAY17	1577	1599	forward 3	TM	Transmembrane
321	U:475378.3:2001MAY17	1600	1612	forward 3	TM	Non-Cytosolic
322	U:749588.15:2001MAY17	1	843	forward 1	TM	Non-Cytosolic
322	U:749588.15:2001MAY17	844	866	forward 1	TM	Transmembrane
322	U:749588.15:2001MAY17	867	1015	forward 1	TM	Cytosolic
322	U:749588.15:2001MAY17	1016	1038	forward 1	TM	Transmembrane
322	U:749588.15:2001MAY17	1039	1278	forward 1	TM	Non-Cytosolic
322	U:749588.15:2001MAY17	1	87	forward 3	TM	Cytosolic
322	U:749588.15:2001MAY17	88	110	forward 3	TM	Transmembrane
322	U:749588.15:2001MAY17	111	762	forward 3	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
322	U:749588.15:2001MAY17	763	785	forward 3	TM	Transmembrane
322	U:749588.15:2001MAY17	786	926	forward 3	TM	Cytosolic
322	U:749588.15:2001MAY17	927	949	forward 3	TM	Transmembrane
322	U:749588.15:2001MAY17	950	1278	forward 3	TM	Non-Cytosolic
323	U:757736.17:2001MAY17	1	1369	forward 1	TM	Non-Cytosolic
323	U:757736.17:2001MAY17	1370	1392	forward 1	TM	Transmembrane
323	U:757736.17:2001MAY17	1393	1398	forward 1	TM	Cytosolic
323	U:757736.17:2001MAY17	1399	1421	forward 1	TM	Transmembrane
323	U:757736.17:2001MAY17	1422	1546	forward 1	TM	Non-Cytosolic
323	U:757736.17:2001MAY17	1547	1569	forward 1	TM	Transmembrane
323	U:757736.17:2001MAY17	1570	1731	forward 1	TM	Cytosolic
323	U:757736.17:2001MAY17	1732	1754	forward 1	TM	Transmembrane
323	U:757736.17:2001MAY17	1755	2211	forward 1	TM	Non-Cytosolic
323	U:757736.17:2001MAY17	1	1415	forward 2	TM	Non-Cytosolic
323	U:757736.17:2001MAY17	1416	1438	forward 2	TM	Transmembrane
323	U:757736.17:2001MAY17	1439	1520	forward 2	TM	Cytosolic
323	U:757736.17:2001MAY17	1521	1543	forward 2	TM	Transmembrane
323	U:757736.17:2001MAY17	1544	1552	forward 2	TM	Non-Cytosolic
323	U:757736.17:2001MAY17	1553	1575	forward 2	TM	Transmembrane
323	U:757736.17:2001MAY17	1576	1595	forward 2	TM	Cytosolic
323	U:757736.17:2001MAY17	1596	1618	forward 2	TM	Transmembrane
323	U:757736.17:2001MAY17	1619	2210	forward 2	TM	Non-Cytosolic
323	U:757736.17:2001MAY17	1	1418	forward 3	TM	Non-Cytosolic
323	U:757736.17:2001MAY17	1419	1441	forward 3	TM	Transmembrane
323	U:757736.17:2001MAY17	1442	1530	forward 3	TM	Cytosolic
323	U:757736.17:2001MAY17	1531	1553	forward 3	TM	Transmembrane
323	U:757736.17:2001MAY17	1554	1644	forward 3	TM	Non-Cytosolic
323	U:757736.17:2001MAY17	1645	1664	forward 3	TM	Transmembrane
323	U:757736.17:2001MAY17	1665	1731	forward 3	TM	Cytosolic
323	U:757736.17:2001MAY17	1732	1754	forward 3	TM	Transmembrane
323	U:757736.17:2001MAY17	1755	1836	forward 3	TM	Non-Cytosolic
323	U:757736.17:2001MAY17	1837	1859	forward 3	TM	Transmembrane
323	U:757736.17:2001MAY17	1860	1986	forward 3	TM	Cytosolic
323	U:757736.17:2001MAY17	1987	2004	forward 3	TM	Transmembrane
323	U:757736.17:2001MAY17	2005	2160	forward 3	TM	Non-Cytosolic
323	U:757736.17:2001MAY17	2161	2180	forward 3	TM	Transmembrane
323	U:757736.17:2001MAY17	2181	2210	forward 3	TM	Cytosolic
324	U:817278.4:2001MAY17	1	314	forward 2	TM	Cytosolic
325	U:027320.5:2001MAY17	1	198	forward 1	TM	Cytosolic
325	U:027320.5:2001MAY17	199	221	forward 1	TM	Transmembrane
325	U:027320.5:2001MAY17	222	279	forward 1	TM	Non-Cytosolic
325	U:027320.5:2001MAY17	280	302	forward 1	TM	Transmembrane
325	U:027320.5:2001MAY17	303	322	forward 1	TM	Cytosolic
325	U:027320.5:2001MAY17	323	345	forward 1	TM	Transmembrane
325	U:027320.5:2001MAY17	346	348	forward 1	TM	Non-Cytosolic
325	U:027320.5:2001MAY17	349	371	forward 1	TM	Transmembrane
325	U:027320.5:2001MAY17	372	429	forward 1	TM	Cytosolic
325	U:027320.5:2001MAY17	1	194	forward 2	TM	Cytosolic
325	U:027320.5:2001MAY17	195	217	forward 2	TM	Transmembrane
325	U:027320.5:2001MAY17	218	241	forward 2	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
325	U:027320.5:2001MAY17	242	264	forward 2	TM	Transmembrane
325	U:027320.5:2001MAY17	265	276	forward 2	TM	Cytosolic
325	U:027320.5:2001MAY17	277	299	forward 2	TM	Transmembrane
325	U:027320.5:2001MAY17	300	341	forward 2	TM	Non-Cytosolic
325	U:027320.5:2001MAY17	342	359	forward 2	TM	Transmembrane
325	U:027320.5:2001MAY17	360	429	forward 2	TM	Cytosolic
326	U:204635.5:2001MAY17	1	4	forward 3	TM	Non-Cytosolic
326	U:204635.5:2001MAY17	5	24	forward 3	TM	Transmembrane
326	U:204635.5:2001MAY17	25	211	forward 3	TM	Cytosolic
326	U:204635.5:2001MAY17	212	231	forward 3	TM	Transmembrane
326	U:204635.5:2001MAY17	232	305	forward 3	TM	Non-Cytosolic
327	U:215532.38:2001MAY17	1	254	forward 2	TM	Non-Cytosolic
327	U:215532.38:2001MAY17	255	277	forward 2	TM	Transmembrane
327	U:215532.38:2001MAY17	278	288	forward 2	TM	Cytosolic
327	U:215532.38:2001MAY17	289	311	forward 2	TM	Transmembrane
327	U:215532.38:2001MAY17	312	490	forward 2	TM	Non-Cytosolic
327	U:215532.38:2001MAY17	1	66	forward 3	TM	Cytosolic
327	U:215532.38:2001MAY17	67	89	forward 3	TM	Transmembrane
327	U:215532.38:2001MAY17	90	98	forward 3	TM	Non-Cytosolic
327	U:215532.38:2001MAY17	99	121	forward 3	TM	Transmembrane
327	U:215532.38:2001MAY17	122	125	forward 3	TM	Cytosolic
327	U:215532.38:2001MAY17	126	143	forward 3	TM	Transmembrane
327	U:215532.38:2001MAY17	144	490	forward 3	TM	Non-Cytosolic
328	U:228319.6:2001MAY17	1	208	forward 3	TM	Cytosolic
328	U:228319.6:2001MAY17	209	231	forward 3	TM	Transmembrane
328	U:228319.6:2001MAY17	232	312	forward 3	TM	Non-Cytosolic
328	U:228319.6:2001MAY17	313	335	forward 3	TM	Transmembrane
328	U:228319.6:2001MAY17	336	363	forward 3	TM	Cytosolic
329	U:236589.24:2001MAY17	1	1304	forward 2	TM	Non-Cytosolic
329	U:236589.24:2001MAY17	1305	1327	forward 2	TM	Transmembrane
329	U:236589.24:2001MAY17	1328	1341	forward 2	TM	Cytosolic
330	U:247444.3:2001MAY17	1	415	forward 1	TM	Non-Cytosolic
330	U:247444.3:2001MAY17	416	433	forward 1	TM	Transmembrane
330	U:247444.3:2001MAY17	434	499	forward 1	TM	Cytosolic
330	U:247444.3:2001MAY17	500	522	forward 1	TM	Transmembrane
330	U:247444.3:2001MAY17	523	541	forward 1	TM	Non-Cytosolic
330	U:247444.3:2001MAY17	542	564	forward 1	TM	Transmembrane
330	U:247444.3:2001MAY17	565	595	forward 1	TM	Cytosolic
330	U:247444.3:2001MAY17	1	46	forward 2	TM	Non-Cytosolic
330	U:247444.3:2001MAY17	47	69	forward 2	TM	Transmembrane
330	U:247444.3:2001MAY17	70	80	forward 2	TM	Cytosolic
330	U:247444.3:2001MAY17	81	98	forward 2	TM	Transmembrane
330	U:247444.3:2001MAY17	99	101	forward 2	TM	Non-Cytosolic
330	U:247444.3:2001MAY17	102	124	forward 2	TM	Transmembrane
330	U:247444.3:2001MAY17	125	329	forward 2	TM	Cytosolic
330	U:247444.3:2001MAY17	330	352	forward 2	TM	Transmembrane
330	U:247444.3:2001MAY17	353	412	forward 2	TM	Non-Cytosolic
330	U:247444.3:2001MAY17	413	435	forward 2	TM	Transmembrane
330	U:247444.3:2001MAY17	436	447	forward 2	TM	Cytosolic
330	U:247444.3:2001MAY17	448	470	forward 2	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
330	U:247444.3:2001MAY17	471	493	forward 2	TM	Non-Cytosolic
330	U:247444.3:2001MAY17	494	516	forward 2	TM	Transmembrane
330	U:247444.3:2001MAY17	517	522	forward 2	TM	Cytosolic
330	U:247444.3:2001MAY17	523	545	forward 2	TM	Transmembrane
330	U:247444.3:2001MAY17	546	594	forward 2	TM	Non-Cytosolic
330	U:247444.3:2001MAY17	1	337	forward 3	TM	Non-Cytosolic
330	U:247444.3:2001MAY17	338	360	forward 3	TM	Transmembrane
330	U:247444.3:2001MAY17	361	451	forward 3	TM	Cytosolic
330	U:247444.3:2001MAY17	452	471	forward 3	TM	Transmembrane
330	U:247444.3:2001MAY17	472	485	forward 3	TM	Non-Cytosolic
330	U:247444.3:2001MAY17	486	508	forward 3	TM	Transmembrane
330	U:247444.3:2001MAY17	509	512	forward 3	TM	Cytosolic
330	U:247444.3:2001MAY17	513	535	forward 3	TM	Transmembrane
330	U:247444.3:2001MAY17	536	539	forward 3	TM	Non-Cytosolic
330	U:247444.3:2001MAY17	540	562	forward 3	TM	Transmembrane
330	U:247444.3:2001MAY17	563	594	forward 3	TM	Cytosolic
331	U:332404.20:2001MAY17	1	1010	forward 3	TM	Non-Cytosolic
331	U:332404.20:2001MAY17	1011	1028	forward 3	TM	Transmembrane
331	U:332404.20:2001MAY17	1029	1072	forward 3	TM	Cytosolic
368	LG:1045509.22:2001JUN22	1	29	forward 2	TM	Cytosolic
368	LG:1045509.22:2001JUN22	30	52	forward 2	TM	Transmembrane
368	LG:1045509.22:2001JUN22	53	66	forward 2	TM	Non-Cytosolic
368	LG:1045509.22:2001JUN22	67	89	forward 2	TM	Transmembrane
368	LG:1045509.22:2001JUN22	90	367	forward 2	TM	Cytosolic
368	LG:1045509.22:2001JUN22	368	390	forward 2	TM	Transmembrane
368	LG:1045509.22:2001JUN22	391	399	forward 2	TM	Non-Cytosolic
368	LG:1045509.22:2001JUN22	400	422	forward 2	TM	Transmembrane
368	LG:1045509.22:2001JUN22	423	720	forward 2	TM	Cytosolic
369	LG:246935.4:2001JUN22	1	11	forward 1	TM	Cytosolic
369	LG:246935.4:2001JUN22	12	34	forward 1	TM	Transmembrane
369	LG:246935.4:2001JUN22	35	438	forward 1	TM	Non-Cytosolic
369	LG:246935.4:2001JUN22	439	461	forward 1	TM	Transmembrane
369	LG:246935.4:2001JUN22	462	481	forward 1	TM	Cytosolic
369	LG:246935.4:2001JUN22	482	504	forward 1	TM	Transmembrane
369	LG:246935.4:2001JUN22	505	977	forward 1	TM	Non-Cytosolic
369	LG:246935.4:2001JUN22	1	12	forward 2	TM	Cytosolic
369	LG:246935.4:2001JUN22	13	35	forward 2	TM	Transmembrane
369	LG:246935.4:2001JUN22	36	39	forward 2	TM	Non-Cytosolic
369	LG:246935.4:2001JUN22	40	59	forward 2	TM	Transmembrane
369	LG:246935.4:2001JUN22	60	71	forward 2	TM	Cytosolic
369	LG:246935.4:2001JUN22	72	94	forward 2	TM	Transmembrane
369	LG:246935.4:2001JUN22	95	880	forward 2	TM	Non-Cytosolic
369	LG:246935.4:2001JUN22	881	903	forward 2	TM	Transmembrane
369	LG:246935.4:2001JUN22	904	976	forward 2	TM	Cytosolic
369	LG:246935.4:2001JUN22	1	12	forward 3	TM	Cytosolic
369	LG:246935.4:2001JUN22	13	35	forward 3	TM	Transmembrane
369	LG:246935.4:2001JUN22	36	869	forward 3	TM	Non-Cytosolic
369	LG:246935.4:2001JUN22	870	892	forward 3	TM	Transmembrane
369	LG:246935.4:2001JUN22	893	976	forward 3	TM	Cytosolic
370	LG:321069.2:2001JUN22	1	630	forward 1	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
370	LG:321069.2:2001JUN22	631	653	forward 1	TM	Transmembrane
370	LG:321069.2:2001JUN22	654	665	forward 1	TM	Cytosolic
370	LG:321069.2:2001JUN22	666	688	forward 1	TM	Transmembrane
370	LG:321069.2:2001JUN22	689	702	forward 1	TM	Non-Cytosolic
370	LG:321069.2:2001JUN22	703	725	forward 1	TM	Transmembrane
370	LG:321069.2:2001JUN22	726	886	forward 1	TM	Cytosolic
370	LG:321069.2:2001JUN22	887	909	forward 1	TM	Transmembrane
370	LG:321069.2:2001JUN22	910	1343	forward 1	TM	Non-Cytosolic
370	LG:321069.2:2001JUN22	1	634	forward 2	TM	Non-Cytosolic
370	LG:321069.2:2001JUN22	635	653	forward 2	TM	Transmembrane
370	LG:321069.2:2001JUN22	654	664	forward 2	TM	Cytosolic
370	LG:321069.2:2001JUN22	665	687	forward 2	TM	Transmembrane
370	LG:321069.2:2001JUN22	688	806	forward 2	TM	Non-Cytosolic
370	LG:321069.2:2001JUN22	807	829	forward 2	TM	Transmembrane
370	LG:321069.2:2001JUN22	830	1078	forward 2	TM	Cytosolic
370	LG:321069.2:2001JUN22	1079	1101	forward 2	TM	Transmembrane
370	LG:321069.2:2001JUN22	1102	1127	forward 2	TM	Non-Cytosolic
370	LG:321069.2:2001JUN22	1128	1150	forward 2	TM	Transmembrane
370	LG:321069.2:2001JUN22	1151	1343	forward 2	TM	Cytosolic
370	LG:321069.2:2001JUN22	1	448	forward 3	TM	Cytosolic
370	LG:321069.2:2001JUN22	449	468	forward 3	TM	Transmembrane
370	LG:321069.2:2001JUN22	469	477	forward 3	TM	Non-Cytosolic
370	LG:321069.2:2001JUN22	478	500	forward 3	TM	Transmembrane
370	LG:321069.2:2001JUN22	501	506	forward 3	TM	Cytosolic
370	LG:321069.2:2001JUN22	507	529	forward 3	TM	Transmembrane
370	LG:321069.2:2001JUN22	530	630	forward 3	TM	Non-Cytosolic
370	LG:321069.2:2001JUN22	631	653	forward 3	TM	Transmembrane
370	LG:321069.2:2001JUN22	654	665	forward 3	TM	Cytosolic
370	LG:321069.2:2001JUN22	666	688	forward 3	TM	Transmembrane
370	LG:321069.2:2001JUN22	689	692	forward 3	TM	Non-Cytosolic
370	LG:321069.2:2001JUN22	693	712	forward 3	TM	Transmembrane
370	LG:321069.2:2001JUN22	713	1070	forward 3	TM	Cytosolic
370	LG:321069.2:2001JUN22	1071	1093	forward 3	TM	Transmembrane
370	LG:321069.2:2001JUN22	1094	1102	forward 3	TM	Non-Cytosolic
370	LG:321069.2:2001JUN22	1103	1122	forward 3	TM	Transmembrane
370	LG:321069.2:2001JUN22	1123	1128	forward 3	TM	Cytosolic
370	LG:321069.2:2001JUN22	1129	1151	forward 3	TM	Transmembrane
370	LG:321069.2:2001JUN22	1152	1343	forward 3	TM	Non-Cytosolic
371	LG:346724.14:2001JUN22	1	380	forward 1	TM	Non-Cytosolic
371	LG:346724.14:2001JUN22	381	400	forward 1	TM	Transmembrane
371	LG:346724.14:2001JUN22	401	497	forward 1	TM	Cytosolic
371	LG:346724.14:2001JUN22	498	520	forward 1	TM	Transmembrane
371	LG:346724.14:2001JUN22	521	599	forward 1	TM	Non-Cytosolic
371	LG:346724.14:2001JUN22	600	622	forward 1	TM	Transmembrane
371	LG:346724.14:2001JUN22	623	877	forward 1	TM	Cytosolic
371	LG:346724.14:2001JUN22	878	900	forward 1	TM	Transmembrane
371	LG:346724.14:2001JUN22	901	948	forward 1	TM	Non-Cytosolic
371	LG:346724.14:2001JUN22	949	971	forward 1	TM	Transmembrane
371	LG:346724.14:2001JUN22	972	1014	forward 1	TM	Cytosolic
371	LG:346724.14:2001JUN22	1015	1037	forward 1	TM	Transmembrane



TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
371	LG:346724.14:2001JUN22	1038	1090	forward 1	TM	Non-Cytosolic
371	LG:346724.14:2001JUN22	1	11	forward 2	TM	Cytosolic
371	LG:346724.14:2001JUN22	12	34	forward 2	TM	Transmembrane
371	LG:346724.14:2001JUN22	35	497	forward 2	TM	Non-Cytosolic
371	LG:346724.14:2001JUN22	498	520	forward 2	TM	Transmembrane
371	LG:346724.14:2001JUN22	521	783	forward 2	TM	Cytosolic
371	LG:346724.14:2001JUN22	784	801	forward 2	TM	Transmembrane
371	LG:346724.14:2001JUN22	802	879	forward 2	TM	Non-Cytosolic
371	LG:346724.14:2001JUN22	880	902	forward 2	TM	Transmembrane
371	LG:346724.14:2001JUN22	903	1090	forward 2	TM	Cytosolic
372	LG:411043.3:2001JUN22	1	121	forward 3	TM	Cytosolic
372	LG:411043.3:2001JUN22	122	144	forward 3	TM	Transmembrane
372	LG:411043.3:2001JUN22	145	203	forward 3	TM	Non-Cytosolic
372	LG:411043.3:2001JUN22	204	223	forward 3	TM	Transmembrane
372	LG:411043.3:2001JUN22	224	458	forward 3	TM	Cytosolic
372	LG:411043.3:2001JUN22	459	481	forward 3	TM	Transmembrane
372	LG:411043.3:2001JUN22	482	707	forward 3	TM	Non-Cytosolic
373	LG:978620.7:2001JUN22	1	490	forward 2	TM	Non-Cytosolic
373	LG:978620.7:2001JUN22	491	513	forward 2	TM	Transmembrane
373	LG:978620.7:2001JUN22	514	515	forward 2	TM	Cytosolic
373	LG:978620.7:2001JUN22	1	351	forward 3	TM	Non-Cytosolic
373	LG:978620.7:2001JUN22	352	374	forward 3	TM	Transmembrane
373	LG:978620.7:2001JUN22	375	514	forward 3	TM	Cytosolic
374	LG:982784.1:2001JUN22	1	315	forward 1	TM	Non-Cytosolic
374	LG:982784.1:2001JUN22	316	338	forward 1	TM	Transmembrane
374	LG:982784.1:2001JUN22	339	358	forward 1	TM	Cytosolic
374	LG:982784.1:2001JUN22	359	381	forward 1	TM	Transmembrane
374	LG:982784.1:2001JUN22	382	682	forward 1	TM	Non-Cytosolic
374	LG:982784.1:2001JUN22	683	705	forward 1	TM	Transmembrane
374	LG:982784.1:2001JUN22	706	715	forward 1	TM	Cytosolic
374	LG:982784.1:2001JUN22	1	359	forward 2	TM	Non-Cytosolic
374	LG:982784.1:2001JUN22	360	382	forward 2	TM	Transmembrane
374	LG:982784.1:2001JUN22	383	715	forward 2	TM	Cytosolic
374	LG:982784.1:2001JUN22	1	227	forward 3	TM	Cytosolic
374	LG:982784.1:2001JUN22	228	246	forward 3	TM	Transmembrane
374	LG:982784.1:2001JUN22	247	255	forward 3	TM	Non-Cytosolic
374	LG:982784.1:2001JUN22	256	278	forward 3	TM	Transmembrane
374	LG:982784.1:2001JUN22	279	358	forward 3	TM	Cytosolic
374	LG:982784.1:2001JUN22	359	376	forward 3	TM	Transmembrane
374	LG:982784.1:2001JUN22	377	398	forward 3	TM	Non-Cytosolic
374	LG:982784.1:2001JUN22	399	421	forward 3	TM	Transmembrane
374	LG:982784.1:2001JUN22	422	433	forward 3	TM	Cytosolic
374	LG:982784.1:2001JUN22	434	456	forward 3	TM	Transmembrane
374	LG:982784.1:2001JUN22	457	475	forward 3	TM	Non-Cytosolic
374	LG:982784.1:2001JUN22	476	498	forward 3	TM	Transmembrane
374	LG:982784.1:2001JUN22	499	715	forward 3	TM	Cytosolic
375	LG:007574.21:2001JUN22	1	6	forward 3	TM	Cytosolic
375	LG:007574.21:2001JUN22	7	29	forward 3	TM	Transmembrane
375	LG:007574.21:2001JUN22	30	38	forward 3	TM	Non-Cytosolic
375	LG:007574.21:2001JUN22	39	56	forward 3	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
375	LG:007574.21:2001JUN22	57	89	forward 3	TM	Cytosolic
375	LG:007574.21:2001JUN22	90	112	forward 3	TM	Transmembrane
375	LG:007574.21:2001JUN22	113	1684	forward 3	TM	Non-Cytosolic
376	LG:013856.18:2001JUN22	1	1178	forward 1	TM	Non-Cytosolic
376	LG:013856.18:2001JUN22	1179	1201	forward 1	TM	Transmembrane
376	LG:013856.18:2001JUN22	1202	1222	forward 1	TM	Cytosolic
376	LG:013856.18:2001JUN22	1	898	forward 2	TM	Non-Cytosolic
376	LG:013856.18:2001JUN22	899	921	forward 2	TM	Transmembrane
376	LG:013856.18:2001JUN22	922	1172	forward 2	TM	Cytosolic
376	LG:013856.18:2001JUN22	1173	1195	forward 2	TM	Transmembrane
376	LG:013856.18:2001JUN22	1196	1221	forward 2	TM	Non-Cytosolic
376	LG:013856.18:2001JUN22	1	11	forward 3	TM	Cytosolic
376	LG:013856.18:2001JUN22	12	34	forward 3	TM	Transmembrane
376	LG:013856.18:2001JUN22	35	1221	forward 3	TM	Non-Cytosolic
377	LG:027320.7:2001JUN22	1	194	forward 2	TM	Cytosolic
377	LG:027320.7:2001JUN22	195	217	forward 2	TM	Transmembrane
377	LG:027320.7:2001JUN22	218	236	forward 2	TM	Non-Cytosolic
377	LG:027320.7:2001JUN22	237	259	forward 2	TM	Transmembrane
377	LG:027320.7:2001JUN22	260	375	forward 2	TM	Cytosolic
377	LG:027320.7:2001JUN22	376	398	forward 2	TM	Transmembrane
377	LG:027320.7:2001JUN22	399	423	forward 2	TM	Non-Cytosolic
377	LG:027320.7:2001JUN22	424	446	forward 2	TM	Transmembrane
377	LG:027320.7:2001JUN22	447	457	forward 2	TM	Cytosolic
377	LG:027320.7:2001JUN22	458	475	forward 2	TM	Transmembrane
377	LG:027320.7:2001JUN22	476	484	forward 2	TM	Non-Cytosolic
377	LG:027320.7:2001JUN22	485	507	forward 2	TM	Transmembrane
377	LG:027320.7:2001JUN22	508	527	forward 2	TM	Cytosolic
377	LG:027320.7:2001JUN22	1	194	forward 3	TM	Cytosolic
377	LG:027320.7:2001JUN22	195	217	forward 3	TM	Transmembrane
377	LG:027320.7:2001JUN22	218	248	forward 3	TM	Non-Cytosolic
377	LG:027320.7:2001JUN22	249	264	forward 3	TM	Transmembrane
377	LG:027320.7:2001JUN22	265	276	forward 3	TM	Cytosolic
377	LG:027320.7:2001JUN22	277	299	forward 3	TM	Transmembrane
377	LG:027320.7:2001JUN22	300	318	forward 3	TM	Non-Cytosolic
377	LG:027320.7:2001JUN22	319	341	forward 3	TM	Transmembrane
377	LG:027320.7:2001JUN22	342	361	forward 3	TM	Cytosolic
377	LG:027320.7:2001JUN22	362	384	forward 3	TM	Transmembrane
377	LG:027320.7:2001JUN22	385	387	forward 3	TM	Non-Cytosolic
377	LG:027320.7:2001JUN22	388	410	forward 3	TM	Transmembrane
377	LG:027320.7:2001JUN22	411	527	forward 3	TM	Cytosolic
378	LG:077967.9:2001JUN22	1	1041	forward 1	TM	Non-Cytosolic
378	LG:077967.9:2001JUN22	1042	1064	forward 1	TM	Transmembrane
378	LG:077967.9:2001JUN22	1065	1078	forward 1	TM	Cytosolic
378	LG:077967.9:2001JUN22	1	757	forward 2	TM	Non-Cytosolic
378	LG:077967.9:2001JUN22	758	780	forward 2	TM	Transmembrane
378	LG:077967.9:2001JUN22	781	1078	forward 2	TM	Cytosolic
379	LG:128475.9:2001JUN22	1	315	forward 2	TM	Non-Cytosolic
379	LG:128475.9:2001JUN22	316	338	forward 2	TM	Transmembrane
379	LG:128475.9:2001JUN22	339	391	forward 2	TM	Cytosolic
379	LG:128475.9:2001JUN22	392	414	forward 2	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
379	LG:128475.9:2001JUN22	415	474	forward 2	TM	Non-Cytosolic
379	LG:128475.9:2001JUN22	475	497	forward 2	TM	Transmembrane
379	LG:128475.9:2001JUN22	498	508	forward 2	TM	Cytosolic
379	LG:128475.9:2001JUN22	509	531	forward 2	TM	Transmembrane
379	LG:128475.9:2001JUN22	532	777	forward 2	TM	Non-Cytosolic
379	LG:128475.9:2001JUN22	778	800	forward 2	TM	Transmembrane
379	LG:128475.9:2001JUN22	801	812	forward 2	TM	Cytosolic
379	LG:128475.9:2001JUN22	813	830	forward 2	TM	Transmembrane
379	LG:128475.9:2001JUN22	831	1065	forward 2	TM	Non-Cytosolic
379	LG:128475.9:2001JUN22	1	495	forward 3	TM	Non-Cytosolic
379	LG:128475.9:2001JUN22	496	518	forward 3	TM	Transmembrane
379	LG:128475.9:2001JUN22	519	524	forward 3	TM	Cytosolic
379	LG:128475.9:2001JUN22	525	547	forward 3	TM	Transmembrane
379	LG:128475.9:2001JUN22	548	1064	forward 3	TM	Non-Cytosolic
380	LG:1398104.15:2001JUN22	1	744	forward 2	TM	Non-Cytosolic
380	LG:1398104.15:2001JUN22	745	767	forward 2	TM	Transmembrane
380	LG:1398104.15:2001JUN22	768	794	forward 2	TM	Cytosolic
380	LG:1398104.15:2001JUN22	1	746	forward 3	TM	Non-Cytosolic
380	LG:1398104.15:2001JUN22	747	769	forward 3	TM	Transmembrane
380	LG:1398104.15:2001JUN22	770	794	forward 3	TM	Cytosolic
381	LG:1454018.10:2001JUN22	1	1296	forward 1	TM	Non-Cytosolic
381	LG:1454018.10:2001JUN22	1297	1319	forward 1	TM	Transmembrane
381	LG:1454018.10:2001JUN22	1320	1331	forward 1	TM	Cytosolic
381	LG:1454018.10:2001JUN22	1332	1351	forward 1	TM	Transmembrane
381	LG:1454018.10:2001JUN22	1352	1472	forward 1	TM	Non-Cytosolic
381	LG:1454018.10:2001JUN22	1	1288	forward 2	TM	Non-Cytosolic
381	LG:1454018.10:2001JUN22	1289	1311	forward 2	TM	Transmembrane
381	LG:1454018.10:2001JUN22	1312	1331	forward 2	TM	Cytosolic
381	LG:1454018.10:2001JUN22	1332	1354	forward 2	TM	Transmembrane
381	LG:1454018.10:2001JUN22	1355	1472	forward 2	TM	Non-Cytosolic
382	LG:221548.14:2001JUN22	1	608	forward 1	TM	Non-Cytosolic
382	LG:221548.14:2001JUN22	609	631	forward 1	TM	Transmembrane
382	LG:221548.14:2001JUN22	632	650	forward 1	TM	Cytosolic
382	LG:221548.14:2001JUN22	651	670	forward 1	TM	Transmembrane
382	LG:221548.14:2001JUN22	671	2297	forward 1	TM	Non-Cytosolic
382	LG:221548.14:2001JUN22	2298	2320	forward 1	TM	Transmembrane
382	LG:221548.14:2001JUN22	2321	2381	forward 1	TM	Cytosolic
382	LG:221548.14:2001JUN22	2382	2404	forward 1	TM	Transmembrane
382	LG:221548.14:2001JUN22	2405	2413	forward 1	TM	Non-Cytosolic
382	LG:221548.14:2001JUN22	2414	2436	forward 1	TM	Transmembrane
382	LG:221548.14:2001JUN22	2437	2498	forward 1	TM	Cytosolic
382	LG:221548.14:2001JUN22	2499	2518	forward 1	TM	Transmembrane
382	LG:221548.14:2001JUN22	2519	2689	forward 1	TM	Non-Cytosolic
382	LG:221548.14:2001JUN22	2690	2712	forward 1	TM	Transmembrane
382	LG:221548.14:2001JUN22	2713	2865	forward 1	TM	Cytosolic
382	LG:221548.14:2001JUN22	2866	2888	forward 1	TM	Transmembrane
382	LG:221548.14:2001JUN22	2889	2990	forward 1	TM	Non-Cytosolic
382	LG:221548.14:2001JUN22	2991	3013	forward 1	TM	Transmembrane
382	LG:221548.14:2001JUN22	3014	3076	forward 1	TM	Cytosolic
382	LG:221548.14:2001JUN22	1	1672	forward 3	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
382	LG:221548.14:2001JUN22	1673	1695	forward 3	TM	Transmembrane
382	LG:221548.14:2001JUN22	1696	1715	forward 3	TM	Cytosolic
382	LG:221548.14:2001JUN22	1716	1735	forward 3	TM	Transmembrane
382	LG:221548.14:2001JUN22	1736	2124	forward 3	TM	Non-Cytosolic
382	LG:221548.14:2001JUN22	2125	2147	forward 3	TM	Transmembrane
382	LG:221548.14:2001JUN22	2148	2299	forward 3	TM	Cytosolic
382	LG:221548.14:2001JUN22	2300	2322	forward 3	TM	Transmembrane
382	LG:221548.14:2001JUN22	2323	3075	forward 3	TM	Non-Cytosolic
383	LG:227500.5:2001JUN22	1	855	forward 1	TM	Non-Cytosolic
383	LG:227500.5:2001JUN22	856	875	forward 1	TM	Transmembrane
383	LG:227500.5:2001JUN22	876	1071	forward 1	TM	Cytosolic
383	LG:227500.5:2001JUN22	1072	1094	forward 1	TM	Transmembrane
383	LG:227500.5:2001JUN22	1095	1120	forward 1	TM	Non-Cytosolic
383	LG:227500.5:2001JUN22	1121	1138	forward 1	TM	Transmembrane
383	LG:227500.5:2001JUN22	1139	1218	forward 1	TM	Cytosolic
383	LG:227500.5:2001JUN22	1219	1238	forward 1	TM	Transmembrane
383	LG:227500.5:2001JUN22	1239	1241	forward 1	TM	Non-Cytosolic
384	LG:228273.22:2001JUN22	1	1379	forward 1	TM	Non-Cytosolic
384	LG:228273.22:2001JUN22	1380	1402	forward 1	TM	Transmembrane
384	LG:228273.22:2001JUN22	1403	1539	forward 1	TM	Cytosolic
384	LG:228273.22:2001JUN22	1	45	forward 3	TM	Cytosolic
384	LG:228273.22:2001JUN22	46	68	forward 3	TM	Transmembrane
384	LG:228273.22:2001JUN22	69	659	forward 3	TM	Non-Cytosolic
384	LG:228273.22:2001JUN22	660	682	forward 3	TM	Transmembrane
384	LG:228273.22:2001JUN22	683	694	forward 3	TM	Cytosolic
384	LG:228273.22:2001JUN22	695	717	forward 3	TM	Transmembrane
384	LG:228273.22:2001JUN22	718	1539	forward 3	TM	Non-Cytosolic
385	LG:235432.1:2001JUN22	1	610	forward 1	TM	Non-Cytosolic
385	LG:235432.1:2001JUN22	611	633	forward 1	TM	Transmembrane
385	LG:235432.1:2001JUN22	634	780	forward 1	TM	Cytosolic
385	LG:235432.1:2001JUN22	1	610	forward 3	TM	Non-Cytosolic
385	LG:235432.1:2001JUN22	611	633	forward 3	TM	Transmembrane
385	LG:235432.1:2001JUN22	634	779	forward 3	TM	Cytosolic
386	LG:236904.20:2001JUN22	1	1425	forward 3	TM	Non-Cytosolic
386	LG:236904.20:2001JUN22	1426	1443	forward 3	TM	Transmembrane
386	LG:236904.20:2001JUN22	1444	1463	forward 3	TM	Cytosolic
386	LG:236904.20:2001JUN22	1464	1486	forward 3	TM	Transmembrane
386	LG:236904.20:2001JUN22	1487	1520	forward 3	TM	Non-Cytosolic
386	LG:236904.20:2001JUN22	1521	1543	forward 3	TM	Transmembrane
386	LG:236904.20:2001JUN22	1544	1570	forward 3	TM	Cytosolic
387	LG:253193.21:2001JUN22	1	6	forward 1	TM	Cytosolic
387	LG:253193.21:2001JUN22	7	29	forward 1	TM	Transmembrane
387	LG:253193.21:2001JUN22	30	920	forward 1	TM	Non-Cytosolic
387	LG:253193.21:2001JUN22	1	159	forward 2	TM	Non-Cytosolic
387	LG:253193.21:2001JUN22	160	182	forward 2	TM	Transmembrane
387	LG:253193.21:2001JUN22	183	259	forward 2	TM	Cytosolic
387	LG:253193.21:2001JUN22	260	282	forward 2	TM	Transmembrane
387	LG:253193.21:2001JUN22	283	920	forward 2	TM	Non-Cytosolic
388	LG:332161.3:2001JUN22	1	631	forward 2	TM	Non-Cytosolic
388	LG:332161.3:2001JUN22	632	654	forward 2	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
388	LG:332161.3:2001JUN22	655	674	forward 2	TM	Cytosolic
388	LG:332161.3:2001JUN22	675	697	forward 2	TM	Transmembrane
388	LG:332161.3:2001JUN22	698	1121	forward 2	TM	Non-Cytosolic
388	LG:332161.3:2001JUN22	1	628	forward 3	TM	Non-Cytosolic
388	LG:332161.3:2001JUN22	629	651	forward 3	TM	Transmembrane
388	LG:332161.3:2001JUN22	652	679	forward 3	TM	Cytosolic
388	LG:332161.3:2001JUN22	680	702	forward 3	TM	Transmembrane
388	LG:332161.3:2001JUN22	703	1121	forward 3	TM	Non-Cytosolic
389	LG:332923.5:2001JUN22	1	1513	forward 1	TM	Non-Cytosolic
389	LG:332923.5:2001JUN22	1514	1536	forward 1	TM	Transmembrane
389	LG:332923.5:2001JUN22	1537	1556	forward 1	TM	Cytosolic
389	LG:332923.5:2001JUN22	1557	1579	forward 1	TM	Transmembrane
389	LG:332923.5:2001JUN22	1580	1644	forward 1	TM	Non-Cytosolic
389	LG:332923.5:2001JUN22	1645	1667	forward 1	TM	Transmembrane
389	LG:332923.5:2001JUN22	1668	1850	forward 1	TM	Cytosolic
389	LG:332923.5:2001JUN22	1851	1873	forward 1	TM	Transmembrane
389	LG:332923.5:2001JUN22	1874	2015	forward 1	TM	Non-Cytosolic
389	LG:332923.5:2001JUN22	2016	2038	forward 1	TM	Transmembrane
389	LG:332923.5:2001JUN22	2039	2041	forward 1	TM	Cytosolic
389	LG:332923.5:2001JUN22	1	1042	forward 2	TM	Non-Cytosolic
389	LG:332923.5:2001JUN22	1043	1065	forward 2	TM	Transmembrane
389	LG:332923.5:2001JUN22	1066	1449	forward 2	TM	Cytosolic
389	LG:332923.5:2001JUN22	1450	1472	forward 2	TM	Transmembrane
389	LG:332923.5:2001JUN22	1473	1555	forward 2	TM	Non-Cytosolic
389	LG:332923.5:2001JUN22	1556	1578	forward 2	TM	Transmembrane
389	LG:332923.5:2001JUN22	1579	1632	forward 2	TM	Cytosolic
389	LG:332923.5:2001JUN22	1633	1655	forward 2	TM	Transmembrane
389	LG:332923.5:2001JUN22	1656	2041	forward 2	TM	Non-Cytosolic
389	LG:332923.5:2001JUN22	1	791	forward 3	TM	Non-Cytosolic
389	LG:332923.5:2001JUN22	792	814	forward 3	TM	Transmembrane
389	LG:332923.5:2001JUN22	815	834	forward 3	TM	Cytosolic
389	LG:332923.5:2001JUN22	835	853	forward 3	TM	Transmembrane
389	LG:332923.5:2001JUN22	854	1326	forward 3	TM	Non-Cytosolic
389	LG:332923.5:2001JUN22	1327	1346	forward 3	TM	Transmembrane
389	LG:332923.5:2001JUN22	1347	1508	forward 3	TM	Cytosolic
389	LG:332923.5:2001JUN22	1509	1528	forward 3	TM	Transmembrane
389	LG:332923.5:2001JUN22	1529	1556	forward 3	TM	Non-Cytosolic
389	LG:332923.5:2001JUN22	1557	1579	forward 3	TM	Transmembrane
389	LG:332923.5:2001JUN22	1580	1633	forward 3	TM	Cytosolic
389	LG:332923.5:2001JUN22	1634	1656	forward 3	TM	Transmembrane
389	LG:332923.5:2001JUN22	1657	2040	forward 3	TM	Non-Cytosolic
390	LG:343500.27:2001JUN22	1	42	forward 2	TM	Cytosolic
390	LG:343500.27:2001JUN22	43	65	forward 2	TM	Transmembrane
390	LG:343500.27:2001JUN22	66	321	forward 2	TM	Non-Cytosolic
391	LG:369703.9:2001JUN22	1	1133	forward 1	TM	Non-Cytosolic
391	LG:369703.9:2001JUN22	1134	1156	forward 1	TM	Transmembrane
391	LG:369703.9:2001JUN22	1157	1157	forward 1	TM	Cytosolic
391	LG:369703.9:2001JUN22	1	224	forward 2	TM	Cytosolic
391	LG:369703.9:2001JUN22	225	247	forward 2	TM	Transmembrane
391	LG:369703.9:2001JUN22	248	1156	forward 2	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain	Topology
392	LG:415378.3:2001JUN22	1	1251	forward 3	TM	Non-Cytosolic
392	LG:415378.3:2001JUN22	1252	1274	forward 3	TM	Transmembrane
392	LG:415378.3:2001JUN22	1275	1355	forward 3	TM	Cytosolic
392	LG:415378.3:2001JUN22	1356	1378	forward 3	TM	Transmembrane
392	LG:415378.3:2001JUN22	1379	1417	forward 3	TM	Non-Cytosolic
392	LG:415378.3:2001JUN22	1418	1440	forward 3	TM	Transmembrane
392	LG:415378.3:2001JUN22	1441	1491	forward 3	TM	Cytosolic
392	LG:415378.3:2001JUN22	1492	1514	forward 3	TM	Transmembrane
392	LG:415378.3:2001JUN22	1515	1851	forward 3	TM	Non-Cytosolic
393	LG:458583.1:2001JUN22	1	108	forward 2	TM	Cytosolic
393	LG:458583.1:2001JUN22	109	131	forward 2	TM	Transmembrane
393	LG:458583.1:2001JUN22	132	323	forward 2	TM	Non-Cytosolic
394	LG:7690373.1:2001JUN22	1	95	forward 2	TM	Cytosolic
394	LG:7690373.1:2001JUN22	96	118	forward 2	TM	Transmembrane
394	LG:7690373.1:2001JUN22	119	219	forward 2	TM	Non-Cytosolic
395	LG:898324.13:2001JUN22	1	225	forward 1	TM	Non-Cytosolic
395	LG:898324.13:2001JUN22	226	248	forward 1	TM	Transmembrane
395	LG:898324.13:2001JUN22	249	276	forward 1	TM	Cytosolic
395	LG:898324.13:2001JUN22	1	189	forward 2	TM	Non-Cytosolic
395	LG:898324.13:2001JUN22	190	212	forward 2	TM	Transmembrane
395	LG:898324.13:2001JUN22	213	224	forward 2	TM	Cytosolic
395	LG:898324.13:2001JUN22	225	247	forward 2	TM	Transmembrane
395	LG:898324.13:2001JUN22	248	276	forward 2	TM	Non-Cytosolic
396	LG:979167.5:2001JUN22	1	252	forward 1	TM	Non-Cytosolic
396	LG:979167.5:2001JUN22	253	272	forward 1	TM	Transmembrane
396	LG:979167.5:2001JUN22	273	344	forward 1	TM	Cytosolic
396	LG:979167.5:2001JUN22	345	362	forward 1	TM	Transmembrane
396	LG:979167.5:2001JUN22	363	366	forward 1	TM	Non-Cytosolic
396	LG:979167.5:2001JUN22	367	386	forward 1	TM	Transmembrane
396	LG:979167.5:2001JUN22	387	627	forward 1	TM	Cytosolic
396	LG:979167.5:2001JUN22	628	647	forward 1	TM	Transmembrane
396	LG:979167.5:2001JUN22	648	661	forward 1	TM	Non-Cytosolic
396	LG:979167.5:2001JUN22	662	684	forward 1	TM	Transmembrane
396	LG:979167.5:2001JUN22	685	708	forward 1	TM	Cytosolic
396	LG:979167.5:2001JUN22	709	731	forward 1	TM	Transmembrane
396	LG:979167.5:2001JUN22	732	1174	forward 1	TM	Non-Cytosolic
396	LG:979167.5:2001JUN22	1175	1194	forward 1	TM	Transmembrane
396	LG:979167.5:2001JUN22	1195	1210	forward 1	TM	Cytosolic
396	LG:979167.5:2001JUN22	1	623	forward 3	TM	Non-Cytosolic
396	LG:979167.5:2001JUN22	624	646	forward 3	TM	Transmembrane
396	LG:979167.5:2001JUN22	647	652	forward 3	TM	Cytosolic
396	LG:979167.5:2001JUN22	653	675	forward 3	TM	Transmembrane
396	LG:979167.5:2001JUN22	676	1209	forward 3	TM	Non-Cytosolic

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1/LG:036272.1:2001MAR30 || 2390-2842; 2435-2838; 2523-2834; 2501-2834; 2531-2833; 2477-2834; 2656-2833; 2490-2834; 2467-2833; 2582-2833; 2406-2834; 2381-2833; 2409-2832; 2371-2833; 2463-2832; 2414-2832; 2447-2832; 2251-2830; 2415-2832; 2718-2832; 2550-2832; 2709-2832; 2524-2832; 2389-2832; 2468-2832; 2488-2832; 2362-2832; 2359-2832; 2394-2832; 2374-2831; 2539-2830; 2424-2832; 2432-2832; 2424-2830; 2442-2830; 2561-2830; 2543-2826; 2423-2828; 2532-2830; 2390-2826; 2636-2821; 2437-2821; 2518-2821; 2351-2813; 2358-2815; 2550-2805; 2524-2804; 2531-2795; 2461-2794; 2513-2793; 2146-2793; 2445-2792; 2445-2791; 2229-2786; 2233-2785; 2361-2784; 2461-2766; 2497-2764; 2301-2764; 2456-2762; 2414-2758; 2332-2747; 2461-2734; 2416-2720; 2495-2719; 2464-2703; 2442-2667; 2077-2647; 2505-2649; 2405-2609; 2025-2597; 2297-2566; 2273-2504; 1885-2484; 2133-2456; 1885-2446; 2217-2416; 1902-2347; 2029-2305; 2057-2303; 2057-2293; 2085-2279; 1812-2238; 1618-2250; 2043-2211; 1968-2198; 1919-2182; 2024-2165; 1697-2148; 1834-2129; 1843-2093; 1823-2060; 1770-2052; 1770-2036; 1825-2015; 1866-2018; 1547-1986; 1652-1882; 1650-1835; 1549-1794; 1066-1597; 535-1163; 141-763; 141-644; 1-218

2/LG:093337.3:2001MAR30 || 1-257; 1-507; 20-487; 29-254; 211-815; 213-475; 309-943; 444-931; 473-1032; 555-986

3/LG:1049927.6:2001MAR30 || 1-323; 16-199; 16-570; 19-664; 20-93; 21-93; 22-93; 176-761; 180-371; 262-842; 282-849; 314-839; 548-943

4/LG:1051891.34:2001MAR30 || 1-491; 325-957; 338-901; 415-901; 420-1016; 435-1017; 461-1023; 577-892; 694-849; 803-1377; 892-1334; 897-1161; 1051-1308; 1078-1330

5/LG:1089626.1:2001MAR30 || 1-210; 1-514; 1-364; 137-689; 137-607; 162-700; 187-775; 243-695; 251-775; 277-775; 295-703; 296-556; 296-519; 298-384; 427-624; 429-800; 484-580; 502-757; 625-967; 627-791; 647-1251; 822-1033; 832-1276; 834-931; 925-1437; 946-1384; 946-1048; 946-1426; 957-1248; 992-1487; 1004-1486; 1014-1317; 1017-1592; 1016-1561; 1017-1536; 1058-1488; 1059-1565; 1076-1365; 1076-1501; 1077-1639; 1087-1568; 1087-1428; 1136-1619; 1136-1616; 1137-1620; 1164-1610; 1169-1610; 1217-1610; 1223-1481; 1228-1581; 1236-1504; 1248-1619; 1248-1621; 1264-1619; 1304-1944; 1299-1944; 1319-1599; 1319-1566; 1328-1620; 1388-1539; 1594-1846; 1594-2082; 1700-2050; 1817-1905; 1898-2427; 1944-2500; 2296-2469; 2319-2537

6/LG:1101416.6:2001MAR30 || 10-442; 1-175; 8-362; 1-409; 8-474; 10-273; 9-256; 10-597; 9-262; 9-251; 9-250; 11-310; 13-398; 9-467; 10-164; 11-166; 13-275; 11-266; 11-295; 12-263; 11-172; 16-267; 12-195; 12-258; 11-284; 13-340; 13-140; 13-205; 13-113; 15-253; 15-302; 13-482; 13-236; 16-260; 15-267; 14-277; 14-283; 17-191; 17-568; 16-572; 15-308; 17-633; 17-288; 17-276; 16-244; 16-178; 15-270; 16-508; 18-168; 20-254; 19-367; 19-291; 17-438; 20-272; 20-261; 20-256; 20-531; 23-277; 28-299; 29-309; 29-284; 31-347; 34-278; 41-280; 42-322; 44-316; 69-216; 71-312; 71-293; 81-282; 80-366; 84-596; 85-296; 89-299; 90-352; 98-268; 139-346; 141-391; 147-598; 148-347; 159-426; 159-384; 160-412; 172-644; 175-412; 179-510; 181-460; 215-423; 222-630; 223-634; 230-633; 242-633; 253-556; 261-630; 277-571; 277-531; 281-525; 292-538; 286-547; 322-671; 335-603; 339-633; 341-633; 345-615; 350-630; 355-582; 358-640; 361-634; 372-633; 373-633; 375-629; 380-635; 387-633; 396-596; 396-657; 404-637; 406-633; 435-633; 440-631; 440-656; 440-897; 455-649; 456-629; 460-631; 462-633; 466-638; 466-633; 472-633; 474-633; 476-634; 476-631; 479-633; 478-633; 480-633; 487-631; 488-632; 488-631; 488-633; 488-654; 492-640; 488-634; 504-638; 504-633; 505-638; 512-633; 537-1058; 556-633; 559-643; 745-1259; 1010-1261; 348-626; 17-349; 376-627; 360-605; 385-622; 385-578; 399-626; 351-579; 374-599; 375-594; 22-239; 346-561; 393-597; 379-580; 9-209; 383-579; 10-205; 16-209; 11-203; 441-625; 8-198; 21-208; 11-197; 23-208; 15-198; 9-183; 9-165; 12-186; 19-189; 14-184; 12-180; 11-179; 8-162; 414-558; 35-182; 28-173; 54-196; 393-536; 12-143; 17-146; 9-137; 9-135; 17-132; 21-132; 46-124

7/LG:1295974.1:2001MAR30 || 414-840; 451-838; 488-838; 550-838; 477-836; 516-837; 541-836; 555-836; 417-835; 731-835; 468-834; 606-832; 407-822;

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 8/LG:1400572.2:2001MAR30 || 1-499; 1-470; 1-385; 1-368  
 9/LG:1446621.1:2001MAR30 || 1-592; 224-609; 266-587; 279-575; 282-674; 284-  
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 10/LG:1499752.1:2001MAR30 || 1-456; 1-355; 24-106; 22-245; 9-225; 7-204;  
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 11/LG:1503044.7:2001MAR30 || 1-605; 8-547; 21-290; 50-645; 127-452; 365-  
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 12/LG:1503588.1:2001MAR30 || 1-296; 12-383  
 13/LG:1503589.2:2001MAR30 || 1-477; 5-246; 139-290; 367-1012; 377-616; 390-  
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 14/LG:1506339.4:2001MAR30 || 1-86; 1-674; 1-241; 1-578; 1-140; 1-254; 22-  
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 15/LG:220648.6:2001MAR30 || 1-256; 1-99; 17-312; 17-331; 35-541; 45-413;  
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 16/LG:236654.1:2001MAR30 || 1-192; 5-330; 6-304; 6-303; 13-98; 14-549; 23-  
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 17/LG:237699.26:2001MAR30 || 1-262; 1-265; 21-253; 21-327; 21-311; 21-310;  
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 18/LG:311541.16:2001MAR30 || 1-599; 23-618; 266-920; 427-892; 428-659; 613-  
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 19/LG:335923.7:2001MAR30 || 304-724; 148-591; 145-590; 213-588; 178-586;  
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 20/LG:350342.14:2001MAR30 || 1-264; 4-158; 6-3089; 25-405; 25-521; 79-683;  
 294-552; 318-600; 361-607; 394-1011; 398-648; 408-910; 451-927; 502-983;  
 507-1021; 514-748; 567-658; 595-683; 612-763; 746-992; 747-1002; 749-1029;  
 762-1237; 806-983; 914-1163; 916-1487; 922-1585; 1057-1531; 1057-1308;  
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 2187-2537; 2188-2434; 2192-2378; 2232-2431; 2243-2323; 2258-2511; 2257-  
 2515; 2299-2501; 2301-2568; 2338-2551; 2350-2557; 2364-2617; 2367-2634;  
 2385-2921; 2386-2641; 2398-2917; 2449-2996; 2471-2975; 2490-2789; 2490-  
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 2657-2940; 2668-2915; 2686-3095; 2697-2836; 2700-2911; 2714-3093; 2732-  
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21/LG:369301.32:2001MAR30 || 8-475; 2-388; 1-197; 42-594; 62-329; 112-574; 147-403; 155-631; 167-766; 182-494; 219-400; 305-556; 428-1003; 448-1038; 382-435; 419-660; 499-1071; 494-751; 507-688; 534-1134; 552-792; 567-866; 572-814; 584-862; 614-866; 628-1080; 641-1081; 667-1103; 698-1142; 699-886; 717-1127; 717-1204; 717-976; 814-1392; 846-1099; 851-1069; 912-1175; 895-1309; 870-1077; 942-1517; 931-1066; 892-1055; 939-1027; 960-1217; 969-1525; 983-1254; 1005-1209; 1015-1552; 1015-1561; 1015-1259; 1022-1456; 1065-1444; 1065-1340; 1070-1319; 1082-1261; 1102-1420; 1140-1284; 1141-1605; 1215-1352; 1134-1306; 1166-1319; 1156-1445; 1162-1596; 1179-1359; 1179-1570; 1190-1598; 1197-1568; 1208-1490; 1209-1491; 1210-1503; 1211-1458; 1206-1598; 1206-1534; 1206-1501; 1208-1602; 1224-1587; 1229-1603; 1248-1854; 1257-1598; 1286-1524; 1287-1497; 1290-1870; 1293-1598; 1310-1598; 1314-1477; 1366-1598; 1385-1896; 1433-1865; 1444-1677; 1444-1675; 1452-1602; 1456-1598; 1540-1884; 1595-1777; 1597-1874; 1597-1777; 1600-1883; 1613-1903; 1634-1874; 1635-1874; 1668-1884; 1738-1874; 1763-1876; 1785-1897; 1823-2121; 1953-2297; 1992-2215; 1995-2246; 2007-2332; 2030-2337; 2037-2334; 2037-2304; 2037-2324; 2037-2094; 2037-2093; 2037-2296; 2037-2299; 2037-2269; 2037-2209; 2037-2189; 2037-2300; 2044-2296; 2134-2719; 2136-2378; 2146-2370; 2202-2703; 2229-2471; 2282-2610; 2284-2740; 2299-2610; 2301-2528; 2307-2610; 2327-2576; 2333-2444; 2333-2715; 2340-2716; 2340-2749; 2340-2708; 2340-2624; 2340-2610; 2340-2621; 2344-2714; 2348-2677; 2378-2677; 2387-2610; 2415-2610; 2436-2962; 2467-2610; 2552-2610; 2571-2810; 2602-2742; 2647-2745; 2761-2870; 2786-3434; 3120-3657; 3140-3662; 3172-3434; 3281-3766; 3294-3827; 3433-3711; 3549-4156; 3603-3840; 3673-4284; 3787-4039; 3802-4039; 3806-4039; 3858-4425; 4116-4709; 4132-4647; 4168-4644

22/LG:452089.1:2001MAR30 || 1-497; 35-576; 66-313; 236-685; 376-781

23/LG:454087.3:2001MAR30 || 1-540; 8-537; 13-528; 251-778; 283-735; 339-717; 700-1272; 704-1254; 829-1387; 897-1445; 1309-1876; 1375-1739; 1394-1687; 1394-1624

24/LG:466302.1:2001MAR30 || 1-529; 16-107; 18-542; 24-131; 101-542

25/LG:474267.1:2001MAR30 || 1-273; 7-275; 195-382; 195-408; 195-435; 197-463; 197-458; 200-486; 202-588; 201-426; 201-429; 202-455; 202-719; 204-494; 203-481; 203-499; 208-469; 209-493; 209-436; 210-475; 212-478; 215-500; 215-478; 218-403; 218-419; 219-468; 219-634; 222-428; 223-376; 225-767; 225-473; 226-515; 227-395; 226-477; 227-477; 230-466; 230-454; 230-481; 231-475; 233-462; 232-546; 234-499; 234-560; 234-885; 236-484; 237-497; 237-826; 237-853; 240-700; 237-827; 240-440; 241-526; 241-496; 255-744; 247-477; 247-527; 248-516; 252-670; 252-606; 251-593; 254-520; 256-655; 260-503; 261-551; 265-676; 264-495; 264-493; 265-636; 273-518; 279-751; 288-473; 292-747; 296-532; 349-469; 371-853; 373-851; 373-604; 373-808; 373-617; 377-589; 389-865; 396-859; 396-852; 398-853; 398-852; 400-662; 403-853; 404-823; 407-870; 411-856; 413-855; 415-852; 418-854; 421-855; 420-500; 431-852; 434-853; 442-853; 453-856; 463-853; 465-914; 466-782; 467-855; 468-865; 469-858; 469-914; 469-724; 483-853; 484-858; 487-856; 486-861; 489-851; 490-915; 494-914; 495-858; 532-851; 533-853; 543-858; 544-820; 547-853; 545-647; 549-854; 555-819; 566-853; 600-836; 616-773; 618-914; 704-912; 722-825; 729-853

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27/LG:011843.5:2001MAR30 || 1-518; 448-1156; 847-1432; 954-1502; 1109-1502; 1170-1270; 1185-1499; 1402-1654; 1465-1695; 1513-1766; 1513-1761; 1518-1766; 1556-2188; 1556-2190; 1556-1875; 1960-2149

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29/LG:1004781.3:2001MAR30 || 1-462; 145-456; 145-709; 573-1138; 573-1124; 593-942; 838-1227; 852-1481; 852-1385; 972-1258

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165/LI:197388.10:2001MAY17 || 1170-1400; 1185-1340; 1189-1415; 1190-1422; 1243-1402; 1245-1415; 940-1215; 975-1422; 1169-1415; 1-479; 51-665; 36-602; 36-589; 89-378; 142-351; 165-867; 157-403; 157-415; 195-451; 184-274; 189-418; 210-401; 242-684; 245-684; 281-566; 303-904; 295-578; 322-1141; 338-589; 406-1137; 395-491; 450-1278; 919-1171; 919-1134; 500-1121; 598-828; 612-883; 604-896; 647-933; 647-934; 673-833; 680-771; 685-771; 715-1419; 724-1433; 756-1434; 775-1343; 775-1003; 785-1231; 821-1413; 844-1010; 845-959; 855-1128; 854-1124; 868-1105; 885-1128; 868-1104; 1290-1415; 1315-1415; 1320-1400  
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393/LG:458583.1:2001JUN22 || 1-303; 125-335; 125-680; 383-715; 627-972

394/LG:7690373.1:2001JUN22 || 1-252; 28-191; 28-112; 33-561; 197-659; 345-497; 354-488

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Table 5

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3447-3589; 3480-3574; 3480-3586; 3483-3543; 3499-3586

SEQ ID NO:		Template ID	Tissue Distribution
1		LG:036272.1:2001MAR30	Germ Cells - 20%, Urinary Tract - 17%
2		LG:093337.3:2001MAR30	Cardiovascular System - 47%, Endocrine System - 27%, Hemic and Immune System - 20%
3		LG:1049927.6:2001MAR30	Female Genitalia - 30%, Connective Tissue - 30%, Respiratory System - 22%
4		LG:1051891.34:2001MAR30	Nervous System - 35%, Endocrine System - 24%, Digestive System - 12%, Male Genitalia - 12%, Female Genitalia - 12%
5		LG:1089626.1:2001MAR30	Skin - 14%, Male Genitalia - 13%, Respiratory System - 12%
6		LG:1101416.6:2001MAR30	Skin - 11%
7		LG:1295974.1:2001MAR30	Pancreas - 62%, Digestive System - 14%, Female Genitalia - 12%
8		LG:1400572.2:2001MAR30	Female Genitalia - 100%
9		LG:1446621.1:2001MAR30	Endocrine System - 65%, Urinary Tract - 15%, Female Genitalia - 10%, Nervous System - 10%
10		LG:1499752.1:2001MAR30	Liver - 33%, Cardiovascular System - 26%, Digestive System - 15%, Male Genitalia - 15%
11		LG:1503044.7:2001MAR30	Nervous System - 43%, Male Genitalia - 29%, Digestive System - 29%
12		LG:1503588.1:2001MAR30	Endocrine System - 100%
13		LG:1503589.2:2001MAR30	Exocrine Glands - 42%, Nervous System - 21%, Hemic and Immune System - 16%
14		LG:1506339.4:2001MAR30	Connective Tissue - 54%, Hemic and Immune System - 46%
15		LG:220648.6:2001MAR30	Nervous System - 33%, Exocrine Glands - 27%, Cardiovascular System - 27%
16		LG:236654.1:2001MAR30	Unclassified/Mixed - 33%, Respiratory System - 17%, Digestive System - 10%
17		LG:237699.26:2001MAR30	Connective Tissue - 21%, Female Genitalia - 13%, Cardiovascular System - 13%
18		LG:311541.16:2001MAR30	Germ Cells - 30%, Urinary Tract - 17%, Liver - 12%
19		LG:335923.7:2001MAR30	Germ Cells - 71%, Unclassified/Mixed - 25%
20		LG:350342.14:2001MAR30	Sense Organs - 37%, Nervous System - 14%, Stomatognathic System - 13%
21		LG:369301.32:2001MAR30	Connective Tissue - 16%, Unclassified/Mixed - 13%
22		LG:452089.1:2001MAR30	Nervous System - 100%
23		LG:454087.3:2001MAR30	Hemic and Immune System - 24%, Connective Tissue - 24%, Cardiovascular System - 14%, Endocrine System - 14%
24		LG:466302.1:2001MAR30	Liver - 75%, Respiratory System - 17%
25		LG:474267.1:2001MAR30	Endocrine System - 15%, Urinary Tract - 14%, Germ Cells - 13%
26		LG:995613.10:2001MAR30	Liver - 26%, Urinary Tract - 20%, Respiratory System - 14%
27		LG:011843.5:2001MAR30	Embryonic Structures - 32%, Endocrine System - 32%, Nervous System - 14%
28		LG:075904.32:2001MAR30	Urinary Tract - 29%, Respiratory System - 14%, Nervous System - 13%

SEQ ID NO:	Template ID	Tissue Distribution
29	LG:1004781.3:2001MAR30	Urinary Tract - 38%, Nervous System - 38%, Respiratory System - 25%
30	LG:1041807.8:2001MAR30	Nervous System - 18%, Liver - 17%, Sense Organs - 14%
31	LG:1044448.2:2001MAR30	Unclassified/Mixed - 17%, Urinary Tract - 11%, Germ Cells - 10%
32	LG:1080598.9:2001MAR30	Embryonic Structures - 22%, Liver - 11%
33	LG:1081017.1:2001MAR30	Respiratory System - 15%, Pancreas - 13%
34	LG:1083120.2:2001MAR30	Endocrine System - 67%, Female Genitalia - 33%
35	LG:1097492.12:2001MAR30	Liver - 12%
36	LG:118834.9:2001MAR30	Embryonic Structures - 26%, Germ Cells - 21%, Endocrine System - 12%, Unclassified/Mixed - 12%
37	LG:1227408.25:2001MAR30	Nervous System - 41%, Pancreas - 15%, Respiratory System - 11%, Connective Tissue - 11%, Male Genitalia - 11%
38	LG:1326953.1:2001MAR30	Male Genitalia - 47%, Exocrine Glands - 27%, Urinary Tract - 20%
39	LG:1397821.17:2001MAR30	Female Genitalia - 11%
40	LG:1512507.1:2001MAR30	Liver - 100%
41	LG:196583.5:2001MAR30	Connective Tissue - 46%, Cardiovascular System - 12%
42	LG:198669.1:2001MAR30	Sense Organs - 12%, Nervous System - 11%, Pancreas - 11%
43	LG:202943.1:2001MAR30	Embryonic Structures - 57%, Musculoskeletal System - 11%
44	LG:204724.3:2001MAR30	Urinary Tract - 100%
45	LG:206425.10:2001MAR30	Sense Organs - 30%, Pancreas - 14%, Skin - 11%
46	LG:208190.2:2001MAR30	Germ Cells - 31%, Exocrine Glands - 17%, Urinary Tract - 14%
47	LG:222927.2:2001MAR30	Liver - 14%, Musculoskeletal System - 11%
48	LG:228046.5:2001MAR30	Stomatognathic System - 21%
49	LG:230980.1:2001MAR30	Liver - 38%, Digestive System - 33%, Unclassified/Mixed - 15%
50	LG:236976.2:2001MAR30	Germ Cells - 77%, Unclassified/Mixed - 13%
51	LG:238322.6:2001MAR30	Musculoskeletal System - 25%, Sense Organs - 14%
52	LG:341461.1:2001MAR30	Germ Cells - 39%, Male Genitalia - 26%, Exocrine Glands - 14%
53	LG:354088.1:2001MAR30	Respiratory System - 23%, Liver - 21%, Digestive System - 19%
54	LG:376275.1:2001MAR30	Exocrine Glands - 67%, Hemic and Immune System - 17%, Nervous System - 17%
55	LG:399281.3:2001MAR30	Endocrine System - 27%, Female Genitalia - 19%, Hemic and Immune System - 13%, Digestive System - 13%
56	LG:404921.10:2001MAR30	Endocrine System - 11%
57	LG:444677.34:2001MAR30	Nervous System - 35%, Male Genitalia - 28%, Cardiovascular System - 18%
58	LG:968691.1:2001MAR30	Hemic and Immune System - 100%

SEQ ID NO:	Template ID	TABLE 6 Tissue Distribution
59	LG:983862.1:2001MAR30	Unclassified/Mixed - 15%, Liver - 15%, Nervous System - 12%
60	LG:984130.1:2001MAR30	Embryonic Structures - 30%, Unclassified/Mixed - 10%, Male Genitalia - 10%
61	LG:986291.1:2001MAR30	Hemic and Immune System - 100%
62	LG:045210.8:2001MAR30	Germ Cells - 41%, Skin - 31%, Unclassified/Mixed - 10%
63	LG:229284.39:2001MAR30	Embryonic Structures - 11%, Connective Tissue - 10%, Nervous System - 10%
64	LG:337810.20:2001MAR30	Skin - 38%, Germ Cells - 18%
65	LG:463420.1:2001MAR30	Nervous System - 19%, Skin - 11%
66	LG:1080918.1:2001MAR30	Connective Tissue - 38%, Respiratory System - 14%, Exocrine Glands - 11%, Endocrine System - 11%
67	LG:1093747.15:2001MAR30	Germ Cells - 22%, Embryonic Structures - 14%, Urinary Tract - 11%
68	LG:1096896.47:2001MAR30	Embryonic Structures - 40%, Urinary Tract - 15%, Unclassified/Mixed - 15%
69	LG:1098931.39:2001MAR30	Exocrine Glands - 14%, Germ Cells - 14%, Cardiovascular System - 11%
70	LG:1100823.1:2001MAR30	Liver - 53%, Female Genitalia - 41%
71	LG:1166387.1:2001MAR30	Connective Tissue - 11%, Unclassified/Mixed - 11%
72	LG:1383036.49:2001MAR30	widely distributed
73	LG:1452353.14:2001MAR30	Sense Organs - 25%, Unclassified/Mixed - 11%
74	LG:1452435.15:2001MAR30	Liver - 43%, Musculoskeletal System - 13%
75	LG:1498774.1:2001MAR30	Musculoskeletal System - 75%, Nervous System - 25%
76	LG:197180.1:2001MAR30	Pancreas - 11%, Female Genitalia - 10%
77	LG:199489.1:2001MAR30	Musculoskeletal System - 26%, Unclassified/Mixed - 17%, Germ Cells - 11%
78	LG:201908.3:2001MAR30	Germ Cells - 41%, Unclassified/Mixed - 18%
79	LG:247245.26:2001MAR30	Germ Cells - 28%, Exocrine Glands - 22%
80	LG:256365.2:2001MAR30	Male Genitalia - 31%, Urinary Tract - 12%, Cardiovascular System - 12%, Respiratory System - 12%
81	LG:332923.4:2001MAR30	Nervous System - 23%, Sense Organs - 22%, Germ Cells - 12%
82	LG:335276.1:2001MAR30	Nervous System - 30%, Exocrine Glands - 16%, Urinary Tract - 14%, Connective Tissue - 14%
83	LG:350272.2:2001MAR30	Musculoskeletal System - 18%
84	LG:350921.2:2001MAR30	Liver - 18%, Embryonic Structures - 18%, Digestive System - 16%
85	LG:406568.1:2001MAR30	Stomatognathic System - 49%, Musculoskeletal System - 23%, Cardiovascular System - 21%
86	LG:411043.3:2001MAR30	Pancreas - 18%, Urinary Tract - 14%, Nervous System - 11%, Cardiovascular System - 11%
87	LG:414376.20:2001MAR30	Nervous System - 42%, Pancreas - 15%, Exocrine Glands - 13%
88	LG:457695.1:2001MAR30	Nervous System - 100%
89	LG:902390.2:2001MAR30	Nervous System - 100%

TABLE 6

SEQ ID NO:	Template ID	Tissue Distribution
90	LG:903565.20:2001MAR30	Urinary Tract - 18%, Hemic and Immune System - 15%, Liver - 12%, Nervous System - 12%
91	LG:978182.4:2001MAR30	Unclassified/Mixed - 17%, Germ Cells - 12%, Skin - 12%
92	LG:986827.1:2001MAR30	Male Genitalia - 87%, Digestive System - 13%
93	LG:013792.1:2001MAR30	Germ Cells - 86%
94	LG:018258.1:2001MAR30	Digestive System - 33%, Endocrine System - 33%, Urinary Tract - 25%
95	LG:023126.3:2001MAR30	Hemic and Immune System - 92%
96	LG:023618.1:2001MAR30	Nervous System - 41%, Connective Tissue - 10%
97	LG:030999.1:2001MAR30	Sense Organs - 36%, Embryonic Structures - 18%
98	LG:103508.1:2001MAR30	Embryonic Structures - 46%, Unclassified/Mixed - 21%
99	LG:107976.15:2001MAR30	Nervous System - 13%, Sense Organs - 12%
100	LG:1080096.1:2001MAR30	Sense Organs - 29%, Stomatognathic System - 26%
101	LG:1080275.1:2001MAR30	Musculoskeletal System - 32%, Cardiovascular System - 29%, Endocrine System - 11%
102	LG:1090358.10:2001MAR30	Liver - 13%, Embryonic Structures - 13%, Pancreas - 13%, Male Genitalia - 13%
103	LG:1095833.9:2001MAR30	Unclassified/Mixed - 19%, Embryonic Structures - 15%, Skin - 13%
104	LG:1383121.25:2001MAR30	Nervous System - 15%, Liver - 13%
105	LG:1386609.2:2001MAR30	Liver - 11%, Skin - 10%
106	LG:1398465.1:2001MAR30	Sense Organs - 19%, Embryonic Structures - 10%, Cardiovascular System - 10%
107	LG:1453417.10:2001MAR30	Nervous System - 26%, Skin - 18%
108	LG:147869.3:2001MAR30	Endocrine System - 69%, Nervous System - 31%
109	LG:148485.5:2001MAR30	Exocrine Glands - 48%, Urinary Tract - 28%, Female Genitalia - 16%
110	LG:1501818.12:2001MAR30	Sense Organs - 15%
111	LG:1508275.1:2001MAR30	Liver - 100%
112	LG:1509771.1:2001MAR30	Respiratory System - 100%
113	LG:1512998.13:2001MAR30	Sense Organs - 20%
114	LG:198251.7:2001MAR30	Nervous System - 13%, Embryonic Structures - 11%, Sense Organs - 10%
115	LG:198296.1:2001MAR30	Unclassified/Mixed - 11%, Cardiovascular System - 11%
116	LG:198876.13:2001MAR30	Sense Organs - 11%
117	LG:200704.1:2001MAR30	Liver - 36%, Female Genitalia - 28%, Endocrine System - 16%, Nervous System - 16%
118	LG:206593.3:2001MAR30	Exocrine Glands - 28%, Unclassified/Mixed - 24%, Endocrine System - 14%, Nervous System - 14%
119	LG:223970.11:2001MAR30	Skin - 11%
120	LG:227500.5:2001MAR30	Connective Tissue - 17%, Embryonic Structures - 17%, Cardiovascular System - 11%
121	LG:227722.7:2001MAR30	Pancreas - 39%, Urinary Tract - 30%, Male Genitalia - 17%
122	LG:229105.1:2001MAR30	Nervous System - 36%, Digestive System - 23%



SEQ ID NO:		Template ID	TABLE 6 Tissue Distribution
123		LG:233761.4:2001MAR30	widely distributed
124		LG:234326.67:2001MAR30	Nervous System - 12%, Sense Organs - 10%
125		LG:236056.27:2001MAR30	Skin - 23%
126		LG:253889.31:2001MAR30	Germ Cells - 12%, Female Genitalia - 10%
127		LG:270833.135:2001MAR30	Skin - 22%, Sense Organs - 16%, Pancreas - 11%
128		LG:292613.7:2001MAR30	Unclassified/Mixed - 19%
129		LG:331546.2:2001MAR30	Stomatognathic System - 11%
130		LG:332027.6:2001MAR30	Digestive System - 13%, Nervous System - 12%, Male Genitalia - 10%
131		LG:336998.1:2001MAR30	Hemic and Immune System - 12%, Unclassified/Mixed - 11%
132		LG:338010.8:2001MAR30	Exocrine Glands - 33%, Cardiovascular System - 14%, Connective Tissue - 14%
133		LG:344597.1:2001MAR30	Nervous System - 35%, Germ Cells - 33%, Respiratory System - 11%
134		LG:347361.2:2001MAR30	Germ Cells - 10%
135		LG:349293.17:2001MAR30	Germ Cells - 14%, Hemic and Immune System - 13%, Unclassified/Mixed - 13%
136		LG:410595.19:2001MAR30	Sense Organs - 23%, Germ Cells - 12%
137		LG:411151.35:2001MAR30	Musculoskeletal System - 32%, Cardiovascular System - 29%, Stomatognathic System - 11%
138		LG:411334.8:2001MAR30	Unclassified/Mixed - 15%, Connective Tissue - 14%, Male Genitalia - 12%
139		LG:458583.1:2001MAR30	Nervous System - 100%
140		LG:475378.1:2001MAR30	Respiratory System - 13%
141		LG:481572.1:2001MAR30	Skin - 14%
142		LG:481704.1:2001MAR30	Pancreas - 26%, Hemic and Immune System - 21%, Cardiovascular System - 21%
143		LG:898195.4:2001MAR30	Embryonic Structures - 15%
144		LG:903785.1:2001MAR30	Germ Cells - 24%, Unclassified/Mixed - 15%
145		LG:977454.3:2001MAR30	Embryonic Structures - 17%, Cardiovascular System - 13%
146		LG:977724.12:2001MAR30	Connective Tissue - 15%
147		LG:978215.19:2001MAR30	Sense Organs - 25%, Nervous System - 14%, Unclassified/Mixed - 13%
148		LG:981795.1:2001MAR30	Female Genitalia - 38%, Urinary Tract - 32%, Unclassified/Mixed - 20%
149		LG:982784.1:2001MAR30	Germ Cells - 53%
150		LG:987322.4:2001MAR30	Unclassified/Mixed - 11%, Embryonic Structures - 11%
151		LG:006242.7:2001MAR30	widely distributed
152		LG:027320.7:2001MAR30	Unclassified/Mixed - 35%, Embryonic Structures - 24%, Cardiovascular System - 11%, Exocrine Glands - 11%
153		LG:147541.44:2001MAR30	widely distributed
154		LG:228319.2:2001MAR30	Musculoskeletal System - 43%, Hemic and Immune System - 29%, Respiratory System - 14%, Digestive System - 14%
155		LG:238754.19:2001MAR30	widely distributed
156		LG:405751.12:2001MAR30	Exocrine Glands - 13%

SEQ ID NO:		Template ID	Tissue Distribution
157		LI:011822.6:2001MAY17	Nervous System - 38%, Cardiovascular System - 25%, Female Genitalia - 16%
159		LI:1169981.13:2001MAY17	Hemic and Immune System - 20%, Embryonic Structures - 18%, Pancreas - 18%
160		LI:1171553.1:2001MAY17	Sense Organs - 19%
161		LI:1183156.3:2001MAY17	Musculoskeletal System - 26%, Respiratory System - 19%, Hemic and Immune System - 19%
162		LI:1188500.6:2001MAY17	Liver - 61%, Unclassified/Mixed - 16%, Female Genitalia - 16%
163		LI:147333.12:2001MAY17	Connective Tissue - 39%, Liver - 25%, Exocrine Glands - 14%
164		LI:147523.7:2001MAY17	Connective Tissue - 58%, Cardiovascular System - 33%
165		LI:197388.10:2001MAY17	Endocrine System - 17%, Skin - 14%, Connective Tissue - 13%
166		LI:2049216.1:2001MAY17	Connective Tissue - 64%, Hemic and Immune System - 27%
167		LI:2051624.2:2001MAY17	Liver - 35%, Endocrine System - 35%, Unclassified/Mixed - 19%
168		LI:2121838.1:2001MAY17	Germ Cells - 56%, Musculoskeletal System - 18%, Exocrine Glands - 13%
169		LI:2122954.8:2001MAY17	Nervous System - 100%
170		LI:2198064.2:2001MAY17	Female Genitalia - 50%, Hemic and Immune System - 50%
171		LI:2206583.1:2001MAY17	Nervous System - 100%
172		LI:235663.6:2001MAY17	Digestive System - 62%, Respiratory System - 23%, Female Genitalia - 15%
173		LI:236386.7:2001MAY17	Stomatognathic System - 23%, Skin - 13%
174		LI:236654.3:2001MAY17	Respiratory System - 23%, Exocrine Glands - 11%, Unclassified/Mixed - 11%, Male Genitalia - 11%
175		LI:256059.46:2001MAY17	Stomatognathic System - 19%
176		LI:279978.22:2001MAY17	Liver - 48%, Urinary Tract - 44%
177		LI:311541.6:2001MAY17	Germ Cells - 35%, Urinary Tract - 31%
178		LI:346123.1:2001MAY17	Exocrine Glands - 71%, Nervous System - 29%
179		LI:381211.5:2001MAY17	Skin - 17%, Sense Organs - 11%
180		LI:412197.82:2001MAY17	Exocrine Glands - 14%
181		LI:412936.49:2001MAY17	Sense Organs - 16%, Germ Cells - 11%, Pancreas - 11%
182		LI:427792.139:2001MAY17	Sense Organs - 13%
183		LI:450229.1:2001MAY17	Nervous System - 100%
185		LI:764701.8:2001MAY17	Hemic and Immune System - 25%, Male Genitalia - 25%, Digestive System - 13%
186		LI:024124.2:2001MAY17	Germ Cells - 62%, Nervous System - 18%, Urinary Tract - 14%
187		LI:038252.3:2001MAY17	Embryonic Structures - 13%, Germ Cells - 12%
188		LI:056882.1:2001MAY17	Exocrine Glands - 63%, Female Genitalia - 25%, Nervous System - 13%
189		LI:059530.1:2001MAY17	Stomatognathic System - 65%, Urinary Tract - 11%

SEQ ID NO:	Template ID	TABLE 6 Tissue Distribution
190	LI:089950.30:2001MAY17	Skin - 31%, Male Genitalia - 15%, Pancreas - 10%
191	LI:1072906.38:2001MAY17	Embryonic Structures - 18%
192	LI:1158936.4:2001MAY17	Musculoskeletal System - 39%, Endocrine System - 28%, Exocrine Glands - 28%
193	LI:1173412.15:2001MAY17	Germ Cells - 31%, Pancreas - 13%
194	LI:1174279.14:2001MAY17	Embryonic Structures - 22%, Liver - 20%, Male Genitalia - 11%
195	LI:1174809.1:2001MAY17	Hemic and Immune System - 86%, Nervous System - 14%
196	LI:1175131.1:2001MAY17	Germ Cells - 23%, Urinary Tract - 21%, Female Genitalia - 12%, Male Genitalia - 12%
197	LI:1188801.10:2001MAY17	Digestive System - 53%, Urinary Tract - 21%, Connective Tissue - 13%
198	LI:1189176.27:2001MAY17	Skin - 59%, Cardiovascular System - 15%
199	LI:197739.4:2001MAY17	Cardiovascular System - 25%, Hemic and Immune System - 17%, Endocrine System - 17%
200	LI:2049016.1:2001MAY17	Unclassified/Mixed - 42%, Embryonic Structures - 42%
201	LI:2049137.1:2001MAY17	Germ Cells - 67%, Unclassified/Mixed - 10%
202	LI:2051907.1:2001MAY17	Digestive System - 38%, Unclassified/Mixed - 31%, Nervous System - 19%
203	LI:2117996.13:2001MAY17	Digestive System - 100%
204	LI:2118683.15:2001MAY17	Unclassified/Mixed - 45%, Germ Cells - 22%, Digestive System - 11%
205	LI:2120312.1:2001MAY17	Embryonic Structures - 43%, Hemic and Immune System - 22%, Respiratory System - 13%
207	LI:2121802.5:2001MAY17	Digestive System - 100%
209	LI:216129.45:2001MAY17	Endocrine System - 14%, Skin - 12%
210	LI:2186630.1:2001MAY17	Endocrine System - 100%
211	LI:2188206.2:2001MAY17	Unclassified/Mixed - 26%, Connective Tissue - 18%, Male Genitalia - 18%
212	LI:2199710.9:2001MAY17	Sense Organs - 78%
213	LI:2209335.2:2001MAY17	Nervous System - 86%, Male Genitalia - 14%
214	LI:230980.13:2001MAY17	Digestive System - 68%, Unclassified/Mixed - 23%
215	LI:244421.37:2001MAY17	Nervous System - 15%, Musculoskeletal System - 13%, Female Genitalia - 13%, Male Genitalia - 13%
216	LI:341998.1:2001MAY17	Unclassified/Mixed - 33%, Hemic and Immune System - 33%, Female Genitalia - 13%, Male Genitalia - 13%
217	LI:347931.10:2001MAY17	Endocrine System - 14%, Digestive System - 11%, Respiratory System - 10%
218	LI:350771.42:2001MAY17	Pancreas - 22%, Male Genitalia - 16%, Digestive System - 11%, Embryonic Structures - 11%
219	LI:354423.6:2001MAY17	Stomatognathic System - 40%, Exocrine Glands - 15%
220	LI:399333.8:2001MAY17	Pancreas - 16%, Germ Cells - 11%
221	LI:445084.36:2001MAY17	Germ Cells - 29%, Cardiovascular System - 23%, Liver - 12%

SEQ ID NO:	Template ID	Tissue Distribution
222	LI:454087.3:2001MAY17	Hemic and Immune System - 41%, Connective Tissue - 32%
223	LI:474887.1:2001MAY17	Unclassified/Mixed - 20%, Sense Organs - 20%, Endocrine System - 12%
224	LI:745251.1:2001MAY17	Hemic and Immune System - 62%, Unclassified/Mixed - 38%
225	LI:747717.9:2001MAY17	Respiratory System - 60%, Digestive System - 40%
226	LI:806211.3:2001MAY17	Nervous System - 44%, Respiratory System - 33%, Male Genitalia - 22%
227	LI:815072.1:2001MAY17	Male Genitalia - 41%, Exocrine Glands - 29%, Urinary Tract - 24%
228	LI:817052.8:2001MAY17	Liver - 14%, Skin - 12%, Sense Organs - 11%, Nervous System - 11%
229	LI:903392.45:2001MAY17	Germ Cells - 33%, Nervous System - 10%
230	LI:013724.1:2001MAY17	Embryonic Structures - 42%, Sense Organs - 26%, Skin - 14%
231	LI:191726.16:2001MAY17	Urinary Tract - 19%, Skin - 19%, Musculoskeletal System - 16%
232	LI:202270.2:2001MAY17	Liver - 42%, Nervous System - 16%, Unclassified/Mixed - 12%
233	LI:2119352.6:2001MAY17	Unclassified/Mixed - 17%, Female Genitalia - 15%, Embryonic Structures - 11%
234	LI:2207776.11:2001MAY17	Digestive System - 20%, Connective Tissue - 14%, Male Genitalia - 12%
235	LI:256442.1:2001MAY17	Respiratory System - 32%, Female Genitalia - 20%, Digestive System - 16%, Cardiovascular System - 16%
237	LI:018494.1:2001MAY17	Urinary Tract - 34%, Endocrine System - 33%, Respiratory System - 19%
238	LI:023518.2:2001MAY17	Urinary Tract - 55%, Musculoskeletal System - 32%, Respiratory System - 14%
239	LI:053488.46:2001MAY17	Urinary Tract - 17%, Musculoskeletal System - 11%, Cardiovascular System - 10%
240	LI:058298.27:2001MAY17	Exocrine Glands - 100%
241	LI:1110046.1:2001MAY17	Liver - 26%, Digestive System - 23%, Unclassified/Mixed - 19%
242	LI:1166752.11:2001MAY17	Embryonic Structures - 20%, Urinary Tract - 12%
243	LI:1173766.1:2001MAY17	Stomatognathic System - 24%, Sense Organs - 21%
244	LI:1177952.4:2001MAY17	Germ Cells - 15%, Skin - 11%, Female Genitalia - 10%
245	LI:1178064.3:2001MAY17	Germ Cells - 40%, Unclassified/Mixed - 16%, Urinary Tract - 11%
246	LI:1183121.1:2001MAY17	Sense Organs - 33%, Pancreas - 23%
247	LI:1190431.13:2001MAY17	Hemic and Immune System - 40%, Pancreas - 12%, Liver - 11%
248	LI:199121.14:2001MAY17	Connective Tissue - 14%, Cardiovascular System - 11%
249	LI:202630.5:2001MAY17	Liver - 36%, Pancreas - 19%

SEQ ID NO:	Template ID	Tissue Distribution
250	LI:2034488.1:2001MAY17	Digestive System - 29%, Female Genitalia - 25%, Connective Tissue - 25%
251	LI:2051434.8:2001MAY17	Connective Tissue - 63%, Unclassified/Mixed - 14%
252	LI:2118475.9:2001MAY17	Unclassified/Mixed - 28%, Hemic and Immune System - 21%, Connective Tissue - 19%
253	LI:218849.24:2001MAY17	Respiratory System - 11%, Musculoskeletal System - 11%
254	LI:2199824.5:2001MAY17	Male Genitalia - 24%, Cardiovascular System - 19%, Urinary Tract - 19%
255	LI:233018.32:2001MAY17	Embryonic Structures - 16%
256	LI:236295.8:2001MAY17	Urinary Tract - 53%, Unclassified/Mixed - 33%, Hemic and Immune System - 13%
257	LI:286989.14:2001MAY17	Embryonic Structures - 14%, Sense Organs - 10%
258	LI:345320.4:2001MAY17	Hemic and Immune System - 30%, Liver - 18%, Germ Cells - 12%
259	LI:355693.18:2001MAY17	Nervous System - 15%, Respiratory System - 11%
260	LI:359876.1:2001MAY17	Exocrine Glands - 100%
261	LI:406664.32:2001MAY17	Cardiovascular System - 28%, Embryonic Structures - 11%, Liver - 11%
262	LI:410324.1:2001MAY17	Sense Organs - 41%, Endocrine System - 12%
263	LI:414376.12:2001MAY17	Nervous System - 38%, Pancreas - 14%, Exocrine Glands - 12%
264	LI:452089.1:2001MAY17	Nervous System - 100%
265	LI:481614.43:2001MAY17	Nervous System - 12%
266	LI:809605.2:2001MAY17	Sense Organs - 37%, Pancreas - 12%
267	LI:816437.25:2001MAY17	Nervous System - 96%
268	LI:817827.5:2001MAY17	Musculoskeletal System - 78%, Nervous System - 22%
269	LI:002345.15:2001MAY17	Stomatognathic System - 14%
270	LI:022629.5:2001MAY17	Germ Cells - 50%, Unclassified/Mixed - 24%
271	LI:061031.4:2001MAY17	Connective Tissue - 30%, Pancreas - 22%, Nervous System - 22%
272	LI:108232.2:2001MAY17	Liver - 50%, Hemic and Immune System - 16%, Endocrine System - 13%
273	LI:1085493.16:2001MAY17	Skin - 18%, Pancreas - 12%, Embryonic Structures - 11%
274	LI:1085513.2:2001MAY17	Musculoskeletal System - 17%, Unclassified/Mixed - 15%, Nervous System - 12%, Cardiovascular System - 12%
275	LI:1086797.9:2001MAY17	Embryonic Structures - 20%, Stomatognathic System - 13%, Liver - 12%
276	LI:1088446.1:2001MAY17	Embryonic Structures - 25%, Endocrine System - 23%, Nervous System - 13%
277	LI:1133764.3:2001MAY17	Germ Cells - 23%, Unclassified/Mixed - 16%, Urinary Tract - 13%
278	LI:1147614.5:2001MAY17	Musculoskeletal System - 14%, Sense Organs - 13%, Connective Tissue - 13%

SEQ ID NO:	Template ID	Tissue Distribution
279	LI:1181710.1:2001MAY17	Hemic and Immune System - 33%, Male Genitalia - 33%, Nervous System - 33%
280	LI:1183192.1:2001MAY17	Cardiovascular System - 28%, Musculoskeletal System - 23%, Urinary Tract - 20%
281	LI:1188786.15:2001MAY17	Embryonic Structures - 17%, Urinary Tract - 13%
282	LI:145626.1:2001MAY17	Sense Organs - 44%, Respiratory System - 16%, Male Genitalia - 14%
283	LI:147869.3:2001MAY17	Endocrine System - 69%, Nervous System - 31%
284	LI:151747.4:2001MAY17	Male Genitalia - 10%
285	LI:198296.1:2001MAY17	Cardiovascular System - 11%
286	LI:200117.4:2001MAY17	Embryonic Structures - 13%, Unclassified/Mixed - 12%
287	LI:200704.1:2001MAY17	Female Genitalia - 37%, Endocrine System - 26%, Nervous System - 21%
288	LI:2049995.3:2001MAY17	Germ Cells - 29%
289	LI:2052097.2:2001MAY17	Liver - 23%, Skin - 20%, Pancreas - 12%
290	LI:209351.22:2001MAY17	Exocrine Glands - 12%, Connective Tissue - 11%, Pancreas - 11%
291	LI:2120481.1:2001MAY17	Female Genitalia - 21%, Musculoskeletal System - 21%, Connective Tissue - 21%
293	LI:2191585.1:2001MAY17	Liver - 100%
294	LI:2198562.3:2001MAY17	Pancreas - 20%, Hemic and Immune System - 11%
295	LI:2209684.5:2001MAY17	Hemic and Immune System - 27%, Female Genitalia - 23%, Exocrine Glands - 23%
296	LI:222795.28:2001MAY17	widely distributed
297	LI:228273.25:2001MAY17	Nervous System - 16%, Embryonic Structures - 14%, Male Genitalia - 10%
298	LI:232386.31:2001MAY17	Unclassified/Mixed - 14%
299	LI:233089.2:2001MAY17	Female Genitalia - 10%, Liver - 10%
300	LI:240641.10:2001MAY17	Sense Organs - 18%, Germ Cells - 12%
301	LI:243871.4:2001MAY17	Hemic and Immune System - 20%, Nervous System - 20%, Embryonic Structures - 19%
302	LI:245597.7:2001MAY17	Skin - 18%, Hemic and Immune System - 12%
303	LI:256009.31:2001MAY17	Urinary Tract - 24%, Hemic and Immune System - 18%, Endocrine System - 15%, Male Genitalia - 15%, Exocrine Glands - 15%
304	LI:262221.1:2001MAY17	Nervous System - 48%, Endocrine System - 15%
305	LI:332957.8:2001MAY17	Stomatognathic System - 29%, Germ Cells - 18%
306	LI:335352.13:2001MAY17	widely distributed
307	LI:343844.7:2001MAY17	Germ Cells - 69%, Connective Tissue - 22%
308	LI:344528.1:2001MAY17	Pancreas - 22%, Hemic and Immune System - 17%, Unclassified/Mixed - 16%
309	LI:374578.27:2001MAY17	Embryonic Structures - 20%, Sense Organs - 16%, Connective Tissue - 11%
310	LI:381993.13:2001MAY17	Germ Cells - 16%, Cardiovascular System - 15%, Unclassified/Mixed - 15%
311	LI:400373.2:2001MAY17	Exocrine Glands - 12%, Sense Organs - 12%
312	LI:400963.6:2001MAY17	Embryonic Structures - 32%, Endocrine System - 15%, Female Genitalia - 11%, Digestive System - 11%

SEQ ID NO:		Template ID	Tissue Distribution
313		LI:404874.8:2001MAY17	Germ Cells - 37%
314		LI:405158.18:2001MAY17	Germ Cells - 13%, Skin - 10%
315		LI:405889.22:2001MAY17	Pancreas - 15%, Skin - 11%
316		LI:411151.31:2001MAY17	Cardiovascular System - 41%, Musculoskeletal System - 32%
317		LI:411313.51:2001MAY17	Nervous System - 16%, Skin - 14%
318		LI:417127.1:2001MAY17	Connective Tissue - 88%, Nervous System - 13%
319		LI:429817.44:2001MAY17	Germ Cells - 23%, Female Genitalia - 16%, Pancreas - 11%
320		LI:474134.23:2001MAY17	Stomatognathic System - 16%, Liver - 14%
321		LI:475378.3:2001MAY17	Respiratory System - 11%
322		LI:749588.15:2001MAY17	Skin - 18%, Unclassified/Mixed - 15%, Female Genitalia - 13%
323		LI:757736.17:2001MAY17	Stomatognathic System - 11%, Musculoskeletal System - 10%
324		LI:817278.4:2001MAY17	Unclassified/Mixed - 90%
325		LI:027320.5:2001MAY17	Embryonic Structures - 32%, Unclassified/Mixed - 16%, Exocrine Glands - 16%
326		LI:204635.5:2001MAY17	Respiratory System - 37%, Embryonic Structures - 29%, Male Genitalia - 20%
327		LI:215532.38:2001MAY17	Sense Organs - 20%, Pancreas - 14%
328		LI:228319.6:2001MAY17	Musculoskeletal System - 54%, Digestive System - 15%, Hemic and Immune System - 15%, Nervous System - 15%
329		LI:236589.24:2001MAY17	Embryonic Structures - 10%
330		LI:247444.3:2001MAY17	Unclassified/Mixed - 20%, Female Genitalia - 15%, Liver - 12%, Male Genitalia - 12%
331		LI:332404.20:2001MAY17	Endocrine System - 36%, Nervous System - 21%, Digestive System - 14%, Hemic and Immune System - 14%, Female Genitalia - 14%
332		LG:1088459.4:2001JUN22	Female Genitalia - 100%
333		LG:1501495.1:2001JUN22	Unclassified/Mixed - 28%, Nervous System - 23%, Digestive System - 13%
334		LG:334284.10:2001JUN22	Unclassified/Mixed - 60%
335		LG:345279.19:2001JUN22	Sense Organs - 22%, Germ Cells - 21%
336		LG:7689681.1:2001JUN22	Unclassified/Mixed - 35%, Digestive System - 24%, Nervous System - 18%
337		LG:7690093.1:2001JUN22	Stomatognathic System - 80%
338		LG:7690175.3:2001JUN22	Cardiovascular System - 23%, Unclassified/Mixed - 20%, Respiratory System -
339		LG:7697128.1:2001JUN22	Exocrine Glands - 67%, Respiratory System - 33%
340		LG:006394.20:2001JUN22	Sense Organs - 15%, Digestive System - 14%, Germ Cells - 10%
341		LG:1012069.1:2001JUN22	Liver - 85%, Male Genitalia - 10%
342		LG:104533.11:2001JUN22	Pancreas - 35%, Liver - 34%, Digestive System - 13%
343		LG:1045853.23:2001JUN22	Endocrine System - 22%, Digestive System - 14%, Pancreas - 11%, Male Genitalia - 11%

SEQ ID NO:	Template ID	Tissue Distribution
344	LG:1081017.8:2001JUN22	Male Genitalia - 38%, Nervous System - 25%, Hemic and Immune System - 19%, Urinary Tract - 19%
345	LG:1090358.6:2001JUN22	Unclassified/Mixed - 86%, Nervous System - 14%
346	LG:1135312.7:2001JUN22	Unclassified/Mixed - 33%, Male Genitalia - 28%, Pancreas - 23%
347	LG:1328501.2:2001JUN22	Endocrine System - 62%, Exocrine Glands - 19%
348	LG:133095.1:2001JUN22	Unclassified/Mixed - 20%
349	LG:135379.5:2001JUN22	Sense Organs - 56%
350	LG:1365581.3:2001JUN22	Embryonic Structures - 21%, Nervous System - 16%, Male Genitalia - 11%
351	LG:1383156.20:2001JUN22	Respiratory System - 90%
352	LG:1501767.18:2001JUN22	Germ Cells - 24%
353	LG:1501890.8:2001JUN22	Hemic and Immune System - 17%, Urinary Tract - 11%, Cardiovascular System - 11%
354	LG:203434.23:2001JUN22	Exocrine Glands - 20%, Urinary Tract - 17%, Embryonic Structures - 17%
355	LG:204724.5:2001JUN22	Urinary Tract - 99%
356	LG:257107.16:2001JUN22	Skin - 12%
357	LG:353530.4:2001JUN22	Embryonic Structures - 15%, Skin - 14%
358	LG:7683573.3:2001JUN22	Endocrine System - 33%, Male Genitalia - 33%, Respiratory System - 17%, Nervous System - 17%
359	LG:7684224.1:2001JUN22	Liver - 100%
360	LG:7690365.2:2001JUN22	Liver - 28%, Embryonic Structures - 28%, Cardiovascular System - 13%, Exocrine Glands - 13%
361	LG:968691.1:2001JUN22	Hemic and Immune System - 100%
362	LG:983076.7:2001JUN22	Pancreas - 19%, Germ Cells - 11%
363	LG:986291.1:2001JUN22	Hemic and Immune System - 100%
364	LG:990347.41:2001JUN22	Sense Organs - 31%, Embryonic Structures - 14%, Skin - 11%
365	LG:998305.4:2001JUN22	Liver - 30%, Pancreas - 30%, Nervous System - 20%
366	LG:463420.16:2001JUN22	Skin - 16%, Nervous System - 15%, Exocrine Glands - 11%
367	LG:979059.3:2001JUN22	Skin - 25%, Unclassified/Mixed - 20%, Exocrine Glands - 11%
368	LG:1045509.22:2001JUN22	Connective Tissue - 28%, Urinary Tract - 15%, Musculoskeletal System - 13%
369	LG:246935.4:2001JUN22	Germ Cells - 30%
370	LG:321069.2:2001JUN22	Unclassified/Mixed - 13%, Stomatognathic System - 13%, Urinary Tract - 12%
371	LG:346724.14:2001JUN22	Unclassified/Mixed - 17%, Sense Organs - 13%, Embryonic Structures - 10%
372	LG:411043.3:2001JUN22	Pancreas - 15%, Exocrine Glands - 13%, Nervous System - 12%, Urinary Tract - 12%
373	LG:978620.7:2001JUN22	Embryonic Structures - 30%, Unclassified/Mixed - 20%, Digestive System - 13%, Male Genitalia - 13%, Exocrine Glands - 13%
374	LG:982784.1:2001JUN22	Germ Cells - 52%



SEQ ID NO:		Template ID	Tissue Distribution
375		LG:007574.21:2001JUN22	Unclassified/Mixed - 22%, Pancreas - 11%, Digestive System - 10%
376		LG:013856.18:2001JUN22	Skin - 14%, Female Genitalia - 10%
377		LG:027320.7:2001JUN22	Unclassified/Mixed - 27%, Liver - 19%, Embryonic Structures - 19%
378		LG:077967.9:2001JUN22	Germ Cells - 33%, Hemic and Immune System - 10%
379		LG:128475.9:2001JUN22	Unclassified/Mixed - 15%, Musculoskeletal System - 15%, Embryonic Structures - 15%
380		LG:1398104.15:2001JUN22	Germ Cells - 31%, Unclassified/Mixed - 19%
381		LG:1454018.10:2001JUN22	Germ Cells - 15%
382		LG:221548.14:2001JUN22	Germ Cells - 12%, Sense Organs - 12%
383		LG:227500.5:2001JUN22	Connective Tissue - 26%, Embryonic Structures - 15%
384		LG:228273.22:2001JUN22	Unclassified/Mixed - 15%, Nervous System - 15%, Embryonic Structures - 13%
385		LG:235432.1:2001JUN22	Embryonic Structures - 20%, Germ Cells - 15%, Hemic and Immune System - 14%
386		LG:236904.20:2001JUN22	Cardiovascular System - 14%, Skin - 11%
387		LG:253193.21:2001JUN22	Liver - 22%, Embryonic Structures - 12%
388		LG:332161.3:2001JUN22	Nervous System - 32%
389		LG:332923.5:2001JUN22	Sense Organs - 42%, Nervous System - 35%, Embryonic Structures - 15%
390		LG:343500.27:2001JUN22	Unclassified/Mixed - 30%, Embryonic Structures - 21%, Male Genitalia - 14%
391		LG:369703.9:2001JUN22	Urinary Tract - 13%, Nervous System - 12%, Respiratory System - 10%
392		LG:415378.3:2001JUN22	Germ Cells - 18%, Embryonic Structures - 14%, Female Genitalia - 10%
393		LG:458583.1:2001JUN22	Male Genitalia - 50%, Nervous System - 50%
394		LG:7690373.1:2001JUN22	Male Genitalia - 40%, Nervous System - 40%, Hemic and Immune System - 20%
395		LG:898324.13:2001JUN22	Skin - 30%, Unclassified/Mixed - 28%, Connective Tissue - 15%
396		LG:979167.5:2001JUN22	Sense Organs - 17%

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
397	2	273	1385	2203	g12846107	1.00E-113	data source:SPTR, source key:Q9RYW0, evidence:ISS-putative-related to ACYL-COA DEHYDROGENASE, PUTATIVE
397	2	273	1385	2203	g13277578	1.00E-102	Unknown (protein for MGC:5601)
397	2	273	1385	2203	g9948609	4.00E-80	probable acyl-CoA dehydrogenase
398	2	321	53	1015	g12652727	1.00E-31	Unknown (protein for IMAGE:3352566)
398	2	321	53	1015	g1049301	5.00E-26	KRAB zinc finger protein; Method: conceptual translation supplied by
398	2	321	53	1015	g15080547	2.00E-25	Unknown (protein for MGC:21259)
399	3	250	3	752	g16551755	4.00E-49	unnamed protein product
399	3	250	3	752	g12053235	9.00E-46	hypothetical protein
399	3	250	3	752	g7981299	3.00E-45	dJ31316.6 (zinc finger protein 165)
400	1	459	1	1377	g186774	0	zinc finger protein
400	1	459	1	1377	g16306806	0	zinc finger protein 43 (HTF6)
400	1	459	1	1377	g38032	0	ZNF43
401	3	480	3	1442	g16549180	0	unnamed protein product
401	3	480	3	1442	g488555	1.00E-138	zinc finger protein ZNF135
401	3	480	3	1442	g5441615	1.00E-138	zinc finger protein
403	2	227	2	682	g50952	1.00E-104	ferritin heavy subunit (AA 1 - 182)
403	2	227	2	682	g485373	1.00E-104	ferritin heavy chain
403	2	227	2	682	g309232	1.00E-104	ferritin heavy chain
404	1	111	1	333	g14042850	2.00E-21	unnamed protein product
404	1	111	1	333	g12851033	3.00E-11	data source:SPTR, source key:Q9JIB8, evidence:ISS-putative-similar to KRAB
404	1	111	1	333	g12805201	4.00E-11	ZINC FINGER PROTEIN
405	3	202	24	629	g7959207	2.00E-38	Similar to zinc finger protein 97
405	3	202	24	629	g3342002	6.00E-36	KIAA1473 protein
405	3	202	24	629	g16553225	9.00E-35	hematopoietic cell derived zinc finger protein
407	1	197	253	843	g2558516	8.00E-95	unnamed protein product
407	1	197	253	843	g15929821	2.00E-94	Rab5 GDP/GTP exchange factor, Rabex5
407	1	197	253	843	g6013006	2.00E-94	putative Rab5 GDP/GTP exchange factor homologue
408	1	117	1	351	g7959207	1.00E-38	Rab5 GDP/GTP exchange factor homologue
408	1	117	1	351	g3342002	3.00E-36	KIAA1473 protein
408	1	117	1	351	g16553225	4.00E-35	hematopoietic cell derived zinc finger protein

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
409	3	254	327	1088	g16552245	1.00E-148	unnamed protein product
409	3	254	327	1088	g16552172	1.00E-115	unnamed protein product
409	3	254	327	1088	g7239109	1.00E-108	HSPC059
410	2	224	2	673	g34392	1.00E-124	put. LLRep3 protein (AA 1-221)
410	2	224	2	673	g2920833	1.00E-124	ribosomal protein S2
410	2	224	2	673	g18203799	1.00E-124	Unknown (protein for MGC:15956)
411	3	189	210	776	g12310941	1.00E-60	unnamed protein product
411	3	189	210	776	g5059156	2.00E-52	Ly-6/neurotoxin homolog
411	3	189	210	776	g12851336	2.00E-52	Ly6/neurotoxin 1~data source:MGD, source key:MGI:1345180, evidence:ISS~putative
412	1	363	1	1089	g17939572	0	Similar to zinc finger protein 296
412	1	363	1	1089	g12843135	1.00E-135	data source:MGD, source key:MGI:1926956, evidence:ISS~putative~zinc finger protein 296
412	1	363	1	1089	g11602755	1.00E-134	zinc finger protein
413	3	231	3	695	g388168	1.00E-128	Bax beta
413	3	231	3	695	g15559636	2.00E-88	Unknown (protein for MGC:20956)
413	3	231	3	695	g12309964	2.00E-88	Human Bax
414	2	370	155	1264	g15209690	0	unnamed protein product
414	2	370	155	1264	g13676427	1.00E-77	hypothetical protein
414	2	370	155	1264	g14250369	2.00E-39	Unknown (protein for IMAGE:4178394)
415	2	136	2	409	g15717944	3.00E-62	bA14C22.1 (novel protein similar to lysozyme)
415	2	136	2	409	g11990770	2.00E-60	bA534G20.1.1 (novel protein similar to Lysozyme C-1 (1,4-beta-N-acylmuramidase C, EC 3.2.1.17) (isoform 1))
415	2	136	2	409	g18204355	8.00E-60	similar to lysozyme C-1 (1,4-beta-N-acylmuramidase C, EC 3.2.1.17)
416	3	265	198	992	g15079361	6.00E-95	Similar to PCTAIRE-motif protein kinase 3
416	3	265	198	992	g12653035	6.00E-95	Unknown (protein for IMAGE:3357514)
416	3	265	198	992	g297102	2.00E-92	serine/threonine protein kinase
417	1	239	469	1185	g14149068	1.00E-129	hypothetical protein
417	1	239	469	1185	g13929449	1.00E-129	dJ337O18.4 (novel protein)
417	1	239	469	1185	g14719307	1.00E-129	SNX21

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
418	2	207	14	634	g7340874	3.00E-88	ESTs D15590(C0900),D48950(S15542),D22684(C0900) correspond to a region of the predicted gene.~Similar to Arabidopsis thaliana 60S ribosomal protein L11A (L16A). (P42795)
418	2	207	14	634	g10799832	6.00E-87	ribosomal protein L11-like
418	2	207	14	634	g9758681	8.00E-87	ribosomal protein L11-like
419	1	437	106	1416	g2689446	0	R27945_1
419	1	437	106	1416	g16549907	1.00E-146	unnamed protein product
419	1	437	106	1416	g3289985	1.00E-141	KIAA0412
420	1	172	25	540	g57111	4.00E-97	ribosomal protein L22
420	1	172	25	540	g13278090	4.00E-97	ribosomal protein L17
420	1	172	25	540	g12847063	4.00E-97	data source:MGD, source key:MGI:96103, evidence:ISS-hexokinase 1-putative
421	3	191	147	719	g15487218	3.00E-17	MORN-domain protein
421	3	191	147	719	g12323331	7.00E-13	putative phosphatidylinositol-4-phosphate 5-kinase; 11335-7537
421	3	191	147	719	g18491177	7.00E-13	putative phosphatidylinositol-4-phosphate 5-kinase
422	1	281	1027	1869	g6807718	1.00E-129	hypothetical protein
422	1	281	1027	1869	g3641527	1.00E-121	low-density lipoprotein receptor-related protein 5
422	1	281	1027	1869	g3582145	1.00E-121	Lipoprotein Receptor Related Protein 5
423	3	697	3	2093	g10998440	0	EGF-related protein SCUBE1
423	3	697	3	2093	g8052237	0	CEGP1 protein
423	3	697	3	2093	g8052320	0	Cegp1 protein
425	1	474	1	1422	g14794726	0	CUB and sushi multiple domains 1 protein
425	1	474	1	1422	g14787176	0	CSMD1
425	1	474	1	1422	g15620827	1.00E-175	KIAA1884 protein
426	1	714	247	2388	g6808293	0	hypothetical protein
426	1	714	247	2388	g2477513	0	F25965_3
426	1	714	247	2388	g15559435	3.00E-89	Unknown (protein for IMAGE:4300179)
427	3	556	969	2636	g14043803	0	Unknown (protein for MGC:14333)
427	3	556	969	2636	g18654480	0	Unknown (protein for MGC:17396)
427	3	556	969	2636	g14307916	0	myosin phosphatase targeting subunit 3 MYPT3
428	3	524	84	1655	g7019945	1.00E-180	unnamed protein product
428	3	524	84	1655	g12804721	1.00E-140	Unknown (protein for MGC:2663)

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
428	3	524	84	1655	g16552245	1.00E-109	unnamed protein product
429	2	182	245	790	g7768736	4.00E-17	putative gene, ankirin like, possible dual specificity Ser/Thr/Tyr kinase domain
429	2	182	245	790	g6808021	6.00E-17	hypothetical protein
429	2	182	245	790	g14245729	6.00E-17	probable dual-specificity Ser/Thr/Tyr kinase
430	2	270	23	832	g14348588	4.00E-69	KRAB zinc finger protein
430	2	270	23	832	g13752754	1.00E-67	zinc finger 1111
430	2	270	23	832	g10047297	6.00E-67	KIAA1611 protein
431	2	1195	2	3586	g10047329	0	KIAA1626 protein
431	2	1195	2	3586	g18256873	0	Unknown (protein for IMAGE:4016433)
431	2	1195	2	3586	g7022610	0	unnamed protein product
432	1	368	1	1104	g7301264	5.00E-90	CG9996 gene product
432	1	368	1	1104	g15990444	8.00E-78	Unknown (protein for IMAGE:4649498)
432	1	368	1	1104	g3878455	2.00E-11	contains similarity to Pfam domain: PF01501 (Glycosyl transferase family 8), Score=-25.1, E-value=7.4e-05, N=1
434	1	123	115	483	g407466	3.00E-34	QM protein
434	1	123	115	483	g402827	3.00E-34	QM
434	1	123	115	483	g190814	3.00E-34	Wilm's tumor-related protein
435	3	316	96	1043	g12060855	1.00E-173	serologically defined breast cancer antigen NY-BR-96
435	3	316	96	1043	g12847582	1.00E-161	data source:SPTR, source key:Q9H272, evidence:ISS~homolog to SEROLOGICALLY DEFINED BREAST CANCER ANTIGEN NY-BR-96~putative
435	3	316	96	1043	g14249854	7.00E-73	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 2
436	2	169	2	508	g7259240	2.00E-79	unnamed protein product
436	2	169	2	508	g12834293	2.00E-79	data source:MGD, source key:MGI:1891227, evidence:ISS~endothelial differentiation-related factor 1~putative
436	2	169	2	508	g12832255	2.00E-79	data source:MGD, source key:MGI:1891227, evidence:ISS~endothelial differentiation-related factor 1~putative
437	2	454	2	1363	g17483854	0	a disintegrin-like and metalloprotease with thrombospondin type 1 motif 14 precursor
437	2	454	2	1363	g15523694	0	unnamed protein product
437	2	454	2	1363	g1865716	2.00E-56	procollagen I N-proteinase
439	1	882	1	2646	g11177164	0	polydom protein
439	1	882	1	2646	g12060830	1.00E-170	serologically defined breast cancer antigen NY-BR-38

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
439	1	882	1	2646	g14787176	1.00E-117	CSMD1
440	2	496	305	1792	g58491	0	E1b 55k protein (transformation)
440	2	496	305	1792	g209820	0	transformation-associated protein
440	2	496	305	1792	g17105043	1.00E-169	54.7 kDa
441	1	415	367	1611	g15558943	0	guanylate binding protein 4
441	1	415	367	1611	g17512480	1.00E-169	Similar to guanylate nucleotide binding protein 3
441	1	415	367	1611	g1174187	1.00E-168	purine nucleotide binding protein
442	1	473	58	1476	g15559603	0	Unknown (protein for MGC:20847)
442	1	473	58	1476	g4559318	1.00E-128	BC273239_1
442	1	473	58	1476	g15929737	1.00E-128	Similar to zinc finger protein 347
443	1	353	1	1059	g12836052	0	data source:SPTR, source key:Q9H334, evidence:ISS-homolog to FORKHEAD
443	1	353	1	1059	g16877224	1.00E-172	BOX PROTEIN P1~putative
443	1	353	1	1059	g15919272	1.00E-114	Unknown (protein for IMAGE:3885983)
444	3	431	615	1907	g3413918	0	putative forkhead/winged-helix transcription factor
444	3	431	615	1907	g220637	7.00E-53	KIAA0478 protein
444	3	431	615	1907	g53133	3.00E-52	zinc finger protein
445	1	420	16	1275	g12842288	0	mkr3
445	1	420	16	1275	g7303380	4.00E-38	Ank repeat containing protein~data source:PFam, source key:PF00023, evidence:ISS~putative
445	1	420	16	1275	g7293339	1.00E-14	CG13320 gene product
446	3	172	66	581	g3900848	8.00E-77	f gene product
446	3	172	66	581	g5441412	1.00E-20	match to EST AA361117 (NID:g2013436)
446	3	172	66	581	g13620482	8.00E-15	dJ513M9.1 (novel Homeobox domain protein)
447	1	718	1150	3303	g18462030	0	hypothetical protein
447	1	718	1150	3303	g12081909	0	semaphorin Y short isoform 1
447	1	718	1150	3303	g14017955	0	semaphorin Y
448	3	200	243	842	g14334177	1.00E-120	KIAA1869 protein
448	3	200	243	842	g16876924	1.00E-120	beta cysteine string protein
448	3	200	243	842	g12838488	1.00E-110	Unknown (protein for MGC:26226)
451	3	349	3	1049	g6453538	5.00E-86	data source:SPTR, source key:P54101, evidence:ISS~putative~similar to CYSTEINE STRING PROTEIN (CSP)
							hypothetical protein

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
451	3	349	3	1049	g6634025	3.00E-28	KIAA0379 protein
451	3	349	3	1049	g7385113	5.00E-28	ankyrin 1
452	2	1060	107	3286	g16549119	0	FLJ00040 protein
452	2	1060	107	3286	g12053081	0	hypothetical protein
452	2	1060	107	3286	g16741323	0	Similar to hypothetical protein DKFZp434L0718
454	1	216	1	648	g17105197	1.00E-108	kelch-like protein KLHL6
454	1	216	1	648	g10439155	6.00E-33	unnamed protein product
454	1	216	1	648	g6329805	2.00E-26	KIAA1129 protein
455	1	701	139	2241	g14274810	0	unnamed protein product
455	1	701	139	2241	g11691855	0	pak5 protein
455	1	701	139	2241	g9082306	0	p21-activated protein kinase 6
456	2	415	182	1426	g10434090	0	unnamed protein product
456	2	415	182	1426	g12836022	3.00E-59	data source:SPTR, source key:Q9P2N7, evidence: ISS-homolog to HYPOTHETICAL PROTEIN KIAA1309 (FRAGMENT)-putative
456	2	415	182	1426	g7243089	1.00E-58	KIAA1354 protein
457	1	298	1	894	g206734	1.00E-165	ribosomal protein L5
457	1	298	1	894	g57125	1.00E-163	ribosomal protein L5 (AA 1-297)
457	1	298	1	894	g12850263	1.00E-162	data source:MGD, source key:MGI:102854, evidence:ISS-putative-ribosomal protein L5 predicted protein dJ257A7.2
458	1	159	1	477	g2827474	1.00E-87	dJ899C14.1 (novel protein similar to KIAA0680) Q9H4T4 like
458	1	159	1	477	g10241527	2.00E-51	hypothetical protein
458	1	159	1	477	g15485622	2.00E-51	unnamed protein product
459	3	399	1845	3041	g5419859	0	HOTTL protein
459	3	399	1845	3041	g10436084	0	Similar to RIKEN cDNA 2410153K17 gene R30923_1
459	3	399	1845	3041	g6683745	1.00E-176	Unknown (protein for IMAGE:3461982)
460	2	220	2	661	g14603176	1.00E-120	KIAA1502 protein
460	2	220	2	661	g4106984	1.00E-120	cerebral cell adhesion molecule
460	2	220	2	661	g13277582	1.00E-104	unnamed protein product
461	2	594	1535	3316	g7959265	0	unnamed protein product
461	2	594	1535	3316	g5764665	0	
461	2	594	1535	3316	g14035822	0	
462	1	500	1	1500	g16549907	0	

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
462	1	500	1	1500	g2887445	1.00E-160	KIAA0412
462	1	500	1	1500	g3289985	1.00E-160	KIAA0412
463	3	490	492	1961	g13436440	0	Unknown (protein for MGC:4400)
463	3	490	492	1961	g10435411	1.00E-125	unnamed protein product
463	3	490	492	1961	g10442700	1.00E-125	zinc-finger protein ZBRK1
464	2	236	2	709	g12655061	2.00E-90	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)
464	2	236	2	709	g506338	2.00E-90	flavoprotein subunit of complex II
464	2	236	2	709	g347134	6.00E-90	succinate dehydrogenase flavoprotein subunit
465	2	953	4337	7195	g452316	0	acetyl-CoA carboxylase
465	2	953	4337	7195	g2138330	0	acetyl-CoA carboxylase
465	2	953	4337	7195	g3080546	0	acetyl-CoA carboxylase
466	1	128	10	393	g55602	1.00E-37	ad1-antigen
466	1	128	10	393	g5410605	1.00E-37	tetraspanin membrane protein CD63
466	1	128	10	393	g15126559	1.00E-37	Similar to Cd63 antigen
467	2	391	371	1543	g7159799	0	dJ351K20.1.1 (novel C3HC4 type Zinc finger (RING finger) protein (isoform
467	2	391	371	1543	g14042318	0	unnamed protein product
467	2	391	371	1543	g7159800	0	dJ351K20.1.2 (novel C3HC4 type Zinc finger (RING finger) protein (isoform
468	3	324	3	974	g2966650	1.00E-158	hnrnp a1 protein
468	3	324	3	974	g193324	1.00E-158	RNA binding protein
468	3	324	3	974	g1711242	1.00E-158	TIS
469	2	1653	56	5014	g189165	0	GAP-related protein
469	2	1653	56	5014	g292354	0	neurofibromin
469	2	1653	56	5014	g1841314	0	neurofibromin
470	3	1536	906	5513	g178646	0	ankyrin
470	3	1536	906	5513	g28702	0	ankyrin (variant 2.1)
470	3	1536	906	5513	g1845265	0	ankyrin
471	2	184	2	553	g2668738	2.00E-89	translation initiation factor 5A
471	2	184	2	553	g1546919	2.00E-89	translation initiation factor 5A
471	2	184	2	553	g3789948	2.00E-83	translation initiation factor 5A
472	3	184	192	743	g50797	1.00E-58	Elongation factor 1-alpha (AA 1 - 461)
472	3	184	192	743	g927065	2.00E-57	eukaryotic translation elongation factor 1 alpha 1-like 14
472	3	184	192	743	g7649316	2.00E-57	elongation factor 1 alpha



TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
473	2	714	2	2143	g849051	0	cationic amino acid transporter 2
473	2	714	2	2143	g2252786	0	hCAT-2A
473	2	714	2	2143	g476725	0	T-cell early activation protein
474	1	947	34	2874	g6329952	0	KIAA1141 protein
474	1	947	34	2874	g17391340	0	Unknown (protein for MGC:20009)
474	1	947	34	2874	g17981470	0	zinc finger protein ZFP100
475	2	426	353	1630	g16551429	1.00E-161	unnamed protein product
475	2	426	353	1630	g1613848	1.00E-150	zinc finger protein zfp6
475	2	426	353	1630	g14042415	1.00E-132	unnamed protein product
476	3	93	909	1187	g54912	2.00E-43	tropomyosin 5
476	3	93	909	1187	g438878	2.00E-43	tropomyosin
476	3	93	909	1187	g312928	2.00E-43	tropomyosin isoform 6
477	3	1067	15	3215	g14388339	0	hypothetical protein
477	3	1067	15	3215	g9845485	0	protocadherin-9
477	3	1067	15	3215	g13874450	0	hypothetical protein
478	3	345	264	1298	g1477586	1.00E-107	DLX-1
478	3	345	264	1298	g1477588	1.00E-107	DLX-1
478	3	345	264	1298	g1620514	2.00E-91	DLX1
479	1	211	322	954	g12845866	5.00E-73	Zinc finger, C3HC4 type (RING finger) containing protein~data source: Pfam, source key: PF00097, evidence: ISS~putative
479	1	211	322	954	g12833017	3.00E-22	Zinc finger, C3HC4 type (RING finger) containing protein~data source: Pfam, source key: PF00097, evidence: ISS~putative
479	1	211	322	954	g458726	1.00E-17	estrogen responsive finger protein (efp)
480	2	465	278	1672	g16508652	0	unnamed protein product
480	2	465	278	1672	g16508650	0	unnamed protein product
480	2	465	278	1672	g7717310	2.00E-63	human ubiquitin processing protease, EC 3.1.2.15
481	1	536	19	1626	g12656196	1.00E-122	cardiac telomodin
481	1	536	19	1626	g17389801	1.00E-73	Unknown (protein for IMAGE:4291177)
481	1	536	19	1626	g28969	2.00E-72	64 Kd autoantigen
482	3	358	150	1223	g18204012	0	Similar to RIKEN cDNA B830026H24 gene

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
482	3	358	150	1223	g12861800	0	data source:SPTR, source key:P97584, evidence:ISS-homolog to NADP-DEPENDENT LEUKOTRIENE B4 12-HYDROXYDEHYDROGENASE (EC 1.1.1.-)
482	3	358	150	1223	g3878713	5.00E-84	(DITHIOLETHIONE-INDUCIBLE GENE-1)-putative weak similarity with quinone oxidoreductase, contains similarity to Pfam domain: PF00107 (Zinc-binding dehydrogenases), Score=-80.6, E-value=6.2e-06, N=1-cDNA EST yk164b4.5 comes from this gene-cDNA EST yk164b4.3 comes from this gene-cDNA EST yk264f3.5 comes from this gene
483	2	449	1112	2458	g32033	0	put. HBK2 protein (AA 1-529)
483	2	449	1112	2458	g57667	0	put. RCK2 protein (AA 1-530)
483	2	449	1112	2458	g199893	0	murine potassium channel protein
484	2	253	2	760	g18655395	1.00E-111	AT3g13580/K20M4_2
484	2	253	2	760	g14532552	1.00E-111	AT3g13580/K20M4_2
484	2	253	2	760	g11994560	1.00E-111	60S ribosomal protein L7
485	2	100	2	301	g12860912	1.00E-36	data source:SPTR, source key:P07108, evidence:ISS-homolog to ACYL-COA-BINDING PROTEIN (ACBP) (DIAZEPAM BINDING INHIBITOR) (DBI) (ENDOZEPINE) (EP)-putative
485	2	100	2	301	g514280	1.00E-35	diazepam-binding inhibitor
485	2	100	2	301	g765223	3.00E-35	ACBP/DBI
486	1	556	1033	2700	g2330553	0	PACE4A-II
486	1	556	1033	2700	g2281776	0	PACE4A-II
486	1	556	1033	2700	g189532	0	subtilisin-like protease
487	2	695	176	2260	g2827086	0	DNA recombination and repair protein
487	2	695	176	2260	g13324574	0	meiotic recombination 11
487	2	695	176	2260	g3328152	0	endo/exonuclease Mre11
488	2	220	98	757	g12855841	6.00E-76	ADP-ribosylation factor family containing protein--data source:Pfam, source key:PF00025, evidence:ISS-putative
488	2	220	98	757	g17736646	4.00E-41	dJ341D10.2 (similar to ADP ribosylation factor 3)
488	2	220	98	757	g12855722	6.00E-39	ADP-ribosylation factor family containing protein--data source:Pfam, source key:PF00025, evidence:ISS-putative
489	2	63	602	790	g15021881	2.00E-10	hypothetical protein
489	2	63	602	790	g7239109	3.00E-10	HSPC059
489	2	63	602	790	g8575775	4.00E-10	KRAB zinc finger protein

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
490	2	241	2	724	g12832288	1.00E-111	data source:SPTR, source key:O75989, evidence:ISS-homolog to DJ422F24.1 (PUTATIVE NOVEL PROTEIN SIMILAR TO C. ELEGANS C02C2.5)
490	2	241	2	724	g3757719	1.00E-88	(FRAGMENT)-putative
490	2	241	2	724	g7294769	3.00E-44	dJ422F24.1 (PUTATIVE novel protein similar to C. elegans C02C2.5)
491	3	214	3	644	g2276313	6.00E-20	CG6279 gene product
							match: multiple proteins; match: Q08151 P28185 Q01111 Q43554; match: Q08150 Q40195 P20340 Q39222; match: Q40368 P36412 P40393 Q40723;
							match: CE01798 Q38923 Q40191 Q41022; match: Q39433 Q40177 Q40218
							Q08146; match: P10949 P11023 Q16948 Q20337; match: Q25389 P25228
							P20336 P05713; match: P35276 Q08147 P17609 P22128; match: Q15771
491	3	214	3	644	g17939907	2.00E-06	P36410 P35291; GTP-binding
491	3	214	3	644	g310200	9.00E-06	UL36 protein
492	3	196	3	590	g6651438	7.00E-24	proline-rich proteoglycan
492	3	196	3	590	g18043508	3.00E-22	putative N-acetyltransferase Camello 2
492	3	196	3	590	g12833022	3.00E-22	camello-like 4
							camello-like 4~data source:MGD, source key:MG1:1915646,
493	1	273	25	843	g7271471	1.00E-159	evidence:ISS-putative
493	1	273	25	843	g14486426	1.00E-149	Rab-related GTP-binding protein RabJ
493	1	273	25	843	g806722	1.00E-24	Rab-related GTP-binding protein
494	3	293	483	1361	g14039836	1.00E-171	YptC4
494	3	293	483	1361	g13568434	1.00E-171	beta 1,3 N-acetylglucosaminyltransferase Lc3 synthase
494	3	293	483	1361	g14597533	1.00E-171	beta 1,3-N-acetylglucosaminyltransferase 5
495	2	922	692	3457	g4151328	0	unnamed protein product
							high-risk human papilloma viruses E6 oncoproteins targeted protein E6TP1
495	2	922	692	3457	g17128219	0	alpha; putative GAP protein alpha
495	2	922	692	3457	g17128217	0	unnamed protein product
496	1	651	1	1953	g5080758	0	unnamed protein product
496	1	651	1	1953	g15021881	1.00E-177	BC331191_1
496	1	651	1	1953	g3540177	1.00E-176	hypothetical protein
497	1	242	1	726	g13938261	8.00E-89	F23269_2
497	1	242	1	726	g5262557	8.00E-89	Unknown (protein for MGC:15514)
							hypothetical protein

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
497	1	242	1	726	g16552172	3.00E-86	unnamed protein product
498	1	309	685	1611	g3540177	1.00E-109	F23269_2
498	1	309	685	1611	g5080758	1.00E-109	BC331191_1
498	1	309	685	1611	g12855931	4.00E-63	data source:SPTR, source key:P16374, evidence:ISS-putative~similar to ZINC FINGER PROTEIN 60 (ZFP-60) (ZINC FINGER PROTEIN MFG-3)
499	2	1212	518	4153	g5726476	0	transcription factor NFAT5 isoform b
499	2	1212	518	4153	g4240143	0	KIAA0827 protein
499	2	1212	518	4153	g14571715	0	tonicity-responsive enhancer binding protein
500	1	130	121	510	g7582292	3.00E-61	BM-010
500	1	130	121	510	g673433	1.00E-49	protein synthesis initiation factor 4A
500	1	130	121	510	g16198386	1.00E-49	Unknown (protein for MGC:27241)
501	2	665	2	1996	g6330433	0	KIAA1203 protein
501	2	665	2	1996	g18204471	1.00E-106	Unknown (protein for MGC:38313)
501	2	665	2	1996	g7291841	3.00E-52	CG3872 gene product
502	1	221	2410	3072	g5410334	1.00E-129	WSB-1 isoform
502	1	221	2410	3072	g7145106	1.00E-109	WSB1 protein
502	1	221	2410	3072	g6563198	1.00E-109	WSB-1 protein
503	2	2894	2	8683	g9828190	0	FLAMINGO 1
503	2	2894	2	8683	g5832711	0	Flamingo 1
503	2	2894	2	8683	g1655821	0	Similar to D.melanogaster cadherin-related tumor suppressor
504	1	493	1	1479	g16549477	0	unnamed protein product
504	1	493	1	1479	g12214288	6.00E-87	dJ402H5.2 (novel protein similar to worm and fly proteins)
504	1	493	1	1479	g7302178	3.00E-48	CG11212 gene product
505	3	299	3	899	g16768654	4.00E-45	HL01494p
505	3	299	3	899	g7292299	2.00E-42	CG1271 gene product
505	3	299	3	899	g15141022	1.00E-39	probable glycerol kinase, similar to sugar kinases protein
506	3	397	90	1280	g13177623	0	dopamine-responsive protein
506	3	397	90	1280	g13543692	0	COBW-like protein
506	3	397	90	1280	g15488579	0	COBW-like protein
507	2	97	26	316	g57175	4.00E-48	S-100 protein
507	2	97	26	316	g206825	4.00E-48	S100 protein
507	2	97	26	316	g404769	1.00E-47	S100 beta protein

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
508	1	130	1	390	g12804565	3.00E-41	Unknown (protein for IMAGE:2989556)
508	1	130	1	390	g12847848	6.00E-16	data source:SPTR, source key:P22978, evidence:ISS-putative~related to HEAT SHOCK PROTEIN 67B2
508	1	130	1	390	g8063	1.00E-14	heat shock protein
509	1	224	439	1110	g18266358	1.00E-116	RUFY2
509	1	224	439	1110	g15625568	1.00E-116	Run- and FYVE-domain containing protein Rabi1p4R
509	1	224	439	1110	g7959341	1.00E-116	KIAA1537 protein
511	1	420	1	1260	g12853497	0	BTB/POZ domain containing protein~data source:Pfam, source key:PF00651, evidence:ISS-putative
511	1	420	1	1260	g18204103	0	RIKEN cDNA 4930429H24 gene
511	1	420	1	1260	g7019911	0	unnamed protein product
512	1	347	352	1392	g13359199	0	KIAA1663 protein
512	1	347	352	1392	g6469034	0	Tob2
512	1	347	352	1392	g6572197	0	bK223H9.1 (TOB4 (BTG1 family protein))
513	2	303	2	910	g13444976	1.00E-146	unnamed protein product
513	2	303	2	910	g12309630	1.00E-146	bA438B23.1 (neuronal leucine-rich repeat protein)
513	2	303	2	910	g16551759	1.00E-146	unnamed protein product
514	2	153	692	1150	g15928468	2.00E-51	Unknown (protein for MGC:25259)
514	2	153	692	1150	g3953593	2.00E-51	Zinc finger protein s11-6
514	2	153	692	1150	g8050899	7.00E-51	ZNF180
515	3	466	207	1604	g4514554	0	Rod1
515	3	466	207	1604	g13879326	0	Similar to regulator of differentiation (in S. pombe) 1
515	3	466	207	1604	g4514552	0	Rod1
516	2	839	284	2800	g16551917	0	unnamed protein product
516	2	839	284	2800	g16356673	0	LIM protein prickie b
516	2	839	284	2800	g14595658	0	LIM protein prickie
517	2	214	2	643	g18461184	2.00E-60	putative katanin
517	2	214	2	643	g3128218	3.00E-53	putative katanin
517	2	214	2	643	g11071813	9.00E-48	probable katanin-like protein
518	3	390	3	1172	g16554016	0	unnamed protein product
518	3	390	3	1172	g13279059	1.00E-173	fatty acid hydroxylase
518	3	390	3	1172	g12803687	1.00E-173	Unknown (protein for MGC:4282)

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
519	3	490	105	1574	g12407377	0	tripartite motif protein TRIM4 isoform alpha
519	3	490	105	1574	g12407379	0	tripartite motif protein TRIM4 isoform beta
519	3	490	105	1574	g15079952	1.00E-116	Similar to tripartite motif protein 4
520	2	983	773	3721	g4240261	0	KIAA0886 protein
520	2	983	773	3721	g11610575	0	RTN-XL
520	2	983	773	3721	g10039551	0	reticulon 4a
521	1	349	673	1719	g13543110	0	Similar to SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2
521	1	349	673	1719	g2723484	0	BAF60b
521	1	349	673	1719	g2723486	0	BAF60b
522	2	309	98	1024	g189310	1.00E-164	nucleolysin TIAR
522	2	309	98	1024	g14714709	1.00E-163	TIA1 cytotoxic granule-associated RNA-binding protein-like 1
522	2	309	98	1024	g1592563	1.00E-160	RNA binding protein TIAR
523	1	361	124	1206	g12844788	3.00E-67	evidence:NAS-hypothetical protein~putative
523	1	361	124	1206	g12578471	2.00E-31	unnamed protein product
523	1	361	124	1206	g12405785	4.00E-30	unnamed protein product
524	3	478	810	2243	g10241461	1.00E-108	dJ1121G12.1.2 (A novel protein containing a putative PHD finger domain, isoform 2)
524	3	478	810	2243	g13195151	1.00E-108	transcription factor TZP
524	3	478	810	2243	g15030164	2.00E-96	Unknown (protein for IMAGE:3709746)
525	1	516	1	1548	g1401126	0	TAK1 binding protein
525	1	516	1	1548	g5834565	0	dJ407F17.1 (TAK1 binding protein 1))
525	1	516	1	1548	g3057038	0	TAB1
526	3	431	393	1685	g12832845	1.00E-161	Domain of unknown function DUF36 containing protein~data source:Pfam, source key:PF01795, evidence:ISS~putative
526	3	431	393	1685	g10726441	6.00E-65	CG14683 gene product
526	3	431	393	1685	g15291185	6.00E-65	GH10770p
527	3	3478	3	10436	g1490271	0	ALL-1 protein
527	3	3478	3	10436	g184394	0	HRX
527	3	3478	3	10436	g688443	0	ALL-1 protein
528	2	268	284	1087	g12860837	1.00E-163	DHHC zinc finger domain containing protein~data source:Pfam, source key:PF01529, evidence:ISS~putative

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
528	2	268	284	1087	g16769014	4.00E-28	LD14687p
528	2	268	284	1087	g7297775	4.00E-28	Dnz1 gene product
529	1	777	1	2331	g13603398	0	SEZ6L
529	1	777	1	2331	g4886439	0	hypothetical protein
529	1	777	1	2331	g6941613	0	dJ268D13.1.2 (seizure related gene 6 (mouse)-like (KIAA0927) (isoform 2))
530	1	635	1624	3528	g6330900	0	KIAA1255 protein
530	1	635	1624	3528	g2914017	0	Ankhn
530	1	635	1624	3528	g6759376	0	ANKHZN
531	3	788	39	2402	g6330948	0	KIAA1261 protein
531	3	788	39	2402	g7239366	0	groucho-related protein 4
531	3	788	39	2402	g4033595	0	groucho protein
532	1	316	163	1110	g13960126	1.00E-125	Similar to leucine-rich neuronal protein
532	1	316	163	1110	g14714829	1.00E-114	Unknown (protein for IMAGE:4152627)
532	1	316	163	1110	g6808196	2.00E-64	hypothetical protein
533	3	633	3	1901	g5441369	0	ZASP protein
533	3	633	3	1901	g3327040	0	KIAA0613 protein
533	3	633	3	1901	g6969631	0	oracle 2 protein
534	3	537	675	2285	g2851884	0	unnamed protein product
534	3	537	675	2285	g16073993	0	unnamed protein product
534	3	537	675	2285	g1537030	0	LPP
535	1	113	211	549	g6714707	1.00E-52	hypothetical protein
535	1	113	211	549	g16589079	1.00E-52	WD repeat protein BIG-3
535	1	113	211	549	g16359284	1.00E-52	Similar to hypothetical protein
536	1	873	1	2619	g7243105	1.00E-118	KIAA1362 protein
536	1	873	1	2619	g7023688	1.00E-109	unnamed protein product
536	1	873	1	2619	g12855942	1.00E-108	data source:MGD, source key:MGI:1261419, evidence:ISS-ethanol
537	1	689	1	2067	g6331213	0	decreased 4-putative
537	1	689	1	2067	g7023247	1.00E-172	KIAA1268 protein
537	1	689	1	2067	g12751141	6.00E-58	unnamed protein product
538	3	114	279	620	g16553621	3.00E-31	B aggressive lymphoma short isoform
538	3	114	279	620	g7959193	7.00E-31	unnamed protein product
							KIAA1466 protein

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
538	3	114	279	620	g18076262	9.00E-29	Pol protein
539	2	650	74	2023	g4650844	0	Kelch motif containing protein
539	2	650	74	2023	g12314036	0	dJ383J4.1 (A Kelch motif-containing protein)
539	2	650	74	2023	g18044145	0	Unknown (protein for MGC:28950)
540	3	738	246	2459	g7242951	0	KIAA1298 protein
540	3	738	246	2459	g18376659	0	hSSH-1L
540	3	738	246	2459	g18376661	1.00E-179	hSSH-1S
541	1	163	1	489	g12844142	2.00E-69	data source:SPT, source key:Q00277, evidence:ISS~putative~related to GLUTATHIONE PEROXIDASE (EC 1.1.1.9) (GPX)
541	1	163	1	489	g18044310	3.00E-69	RIKEN cDNA 2310016C16 gene
541	1	163	1	489	g14042546	1.00E-45	unnamed protein product
542	1	890	265	2934	g3002588	0	Plenty of SH3s; POSH
542	1	890	265	2934	g10432612	0	unnamed protein product
542	1	890	265	2934	g7959249	0	KIAA1494 protein
543	3	567	498	2198	g9309467	1.00E-136	leucine-rich glioma-inactivated 1 protein precursor
543	3	567	498	2198	g18490910	1.00E-136	leucine-rich, glioma inactivated 1
543	3	567	498	2198	g4091819	1.00E-136	leucine-rich glioma-inactivated protein precursor
544	1	258	205	978	g5410527	1.00E-150	paracellin-1
544	1	258	205	978	g5545337	1.00E-131	claudin-16
544	1	258	205	978	g13926043	1.00E-130	paracellin-1
545	3	221	3	665	g16553391	1.00E-137	unnamed protein product
545	3	221	3	665	g12483900	4.00E-67	zinc finger protein HIT-4
545	3	221	3	665	g14456631	3.00E-44	dJ54B20.4 (novel KRAB box containing C2H2 type zinc finger protein)
546	2	774	2	2323	g7555471	0	sirtuin type 1
546	2	774	2	2323	g11596121	0	SIR2alpha protein
546	2	774	2	2323	g6693711	0	Sir2alpha protein
547	3	526	3	1580	g3970833	0	RPB5 meidating protein
547	3	526	3	1580	g17382188	0	unnamed protein product
547	3	526	3	1580	g9997097	0	unnamed protein product
548	2	276	2	829	g16553765	1.00E-127	unnamed protein product
548	2	276	2	829	g12839186	1.00E-121	data source:SPT, source key:Q9VS60, evidence:ISS~putative~related to CG8576 PROTEIN



TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
548	2	276	2	829	g1072250	5.00E-28	F53B1.2 gene product
549	2	198	164	757	g7023491	6.00E-85	unnamed protein product
549	2	198	164	757	g6899846	6.00E-85	disiplatin resistance-associated overexpressed protein
549	2	198	164	757	g14318590	5.00E-79	Unknown (protein for MGC:7100)
550	1	246	646	1383	g16041142	1.00E-133	hypothetical protein
550	1	246	646	1383	g14017813	1.00E-88	KIAA1798 protein
550	1	246	646	1383	g3811111	2.00E-84	I(3)mbt protein homolog
551	1	182	1	546	g14318767	2.00E-68	hypothetical protein MGC10500
551	1	182	1	546	g13477109	2.00E-68	RIKEN cDNA 0610043B10 gene
551	1	182	1	546	g12833998	2.00E-68	data source:SPTR, source key:Q9ESC7, evidence:ISS~putative~similar to MDGL-1
552	2	471	269	1681	g2343085	0	nuclear antigen H731-like protein
552	2	471	269	1681	g1384078	0	apoptosis-Inducible
552	2	471	269	1681	g3426155	0	TIS
553	3	603	108	1916	g16359265	4.00E-87	Similar to hypothetical protein DKFZp434G2226
553	3	603	108	1916	g2239242	1.00E-86	kinesin-like protein
553	3	603	108	1916	g16151809	1.00E-86	kinesin-like protein Klp5
554	3	306	3	920	g18033747	1.00E-170	myosin IIIB
554	3	306	3	920	g16550592	1.00E-169	unnamed protein product
554	3	306	3	920	g10440888	1.00E-122	myosin heavy chain FM3A
555	2	409	101	1327	g4235144	1.00E-158	BC39498_1
555	2	409	101	1327	g7959207	1.00E-157	KIAA1473 protein
555	2	409	101	1327	g16041769	1.00E-151	Unknown (protein for MGC:23189)
556	3	527	399	1979	g16549180	0	unnamed protein product
556	3	527	399	1979	g488555	1.00E-138	zinc finger protein ZNF135
556	3	527	399	1979	g5441615	1.00E-138	zinc finger protein
557	2	628	209	2092	g16553661	0	unnamed protein product
557	2	628	209	2092	g4164083	0	zinc finger protein EZNF
557	2	628	209	2092	g2970038	0	HKL1
558	3	433	198	1496	g14042513	0	unnamed protein product
558	3	433	198	1496	g12836332	0	data source:SPTR, source key:P93647, evidence:ISS~putative~related to MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-)

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
558	3	433	198	1496	g16508614	0	unnamed protein product
559	2	201	1100	1702	g12654987	4.00E-61	Unknown (protein for MGC:5621)
559	2	201	1100	1702	g10435998	3.00E-60	unnamed protein product
559	2	201	1100	1702	g18314540	3.00E-56	Similar to DKFZP586B1621 protein
560	3	153	99	557	g6018682	1.00E-85	superoxide dismutase-4AP
560	3	153	99	557	g1885354	2.00E-83	superoxide dismutase 4A
560	3	153	99	557	g6018746	2.00E-83	superoxide dismutase-4A
561	2	321	191	1153	g13279311	1.00E-165	Similar to RIKEN cDNA 1500017E18 gene
561	2	321	191	1153	g12837716	1.00E-133	data source:SPTR, source key:Q16775, evidence:ISS-homolog to HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6) (GLYOXALASE II) (GLX II)-putative
561	2	321	191	1153	g14336718	1.00E-124	similar to HAGH
562	2	260	2	781	g15866260	1.00E-148	MIRIP2
562	2	260	2	781	g5689535	1.00E-136	KIAA1099 protein
562	2	260	2	781	g15625584	1.00E-136	centaurin gamma2
563	3	340	45	1064	g14602654	0	Unknown (protein for MGC:15400)
563	3	340	45	1064	g18128747	0	unnamed protein product
563	3	340	45	1064	g18128749	0	unnamed protein product
564	3	187	3	563	g16552172	1.00E-114	unnamed protein product
564	3	187	3	563	g16552245	2.00E-81	unnamed protein product
564	3	187	3	563	g498721	2.00E-79	unnamed protein product
565	1	185	541	1095	g16550881	3.00E-91	zinc finger protein
565	1	185	541	1095	g10435738	2.00E-84	unnamed protein product
565	1	185	541	1095	g6088100	3.00E-77	zinc finger protein (ZFD25)
566	3	88	3	266	g12652727	1.00E-29	Unknown (protein for IMAGE:3352566)
566	3	88	3	266	g7020166	2.00E-29	unnamed protein product
566	3	88	3	266	g5679450	2.00E-29	dJ153G14.3 (novel C2H2 type Zinc Finger protein)
567	3	209	3	629	g16553223	7.00E-55	unnamed protein product
567	3	209	3	629	g15488954	1.00E-35	Unknown (protein for MGC:8872)
567	3	209	3	629	g15080235	1.00E-35	Similar to zinc finger protein 113
568	3	298	12	905	g16973457	3.00E-56	beta-3-galactosyltransferase
568	3	298	12	905	g14290592	2.00E-54	beta-1,3-N-acetylglucosaminyltransferase 1

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
568	3	298	12	905	g15421160	2.00E-54	beta-1,3-N-acetylglucosaminyltransferase
569	2	413	1025	2263	g17511850	1.00E-170	Unknown (protein for MGC:32065)
569	2	413	1025	2263	g15042691	2.00E-88	sorting nexin 18
569	2	413	1025	2263	g15559064	2.00E-74	SNAG1
570	3	361	3	1085	g17939572	0	Similar to zinc finger protein 296
570	3	361	3	1085	g11602755	1.00E-134	zinc finger protein
570	3	361	3	1085	g12843135	1.00E-134	data source:MGD, source key:MGI:1926956, evidence:ISS-putative-zinc finger protein 296
571	1	295	22	906	g306852	1.00E-116	HLA-E class I protein precursor
571	1	295	22	906	g15277235	1.00E-116	Class Ib gene, CD94/NKG2 ligand
571	1	295	22	906	g13279158	1.00E-116	Unknown (protein for IMAGE:3622619)
572	2	541	2	1624	g3127193	0	kidney-specific protein
572	2	541	2	1624	g16553412	0	unnamed protein product
572	2	541	2	1624	g5070357	0	xenobiotic/medium-chain fatty acid:CoA ligase form XL-III
573	3	371	141	1253	g15209690	0	unnamed protein product
573	3	371	141	1253	g13676427	1.00E-126	hypothetical protein
573	3	371	141	1253	g9558479	8.00E-21	cysteine-rich protease inhibitor
574	2	282	2	847	g217974	1.00E-143	triosephosphate isomerase
574	2	282	2	847	g168647	1.00E-143	triosephosphate isomerase 1
574	2	282	2	847	g169821	1.00E-128	triosephosphate isomerase
575	3	330	1296	2285	g14042682	4.00E-19	unnamed protein product
575	3	330	1296	2285	g15080180	9.00E-16	Unknown (protein for MGC:20504)
575	3	330	1296	2285	g13160045	9.00E-16	dJ734P14.5 (novel C2H2 type zinc finger protein)
576	2	139	1250	1666	g553841	4.00E-49	ribosomal protein S2
576	2	139	1250	1666	g34392	4.00E-49	put. LLRep3 protein (AA 1-221)
576	2	139	1250	1666	g2920833	4.00E-49	ribosomal protein S2
577	1	213	64	702	g4995305	3.00E-88	PQBP-1 protein
577	1	213	64	702	g4586431	3.00E-88	nuclear protein containing a WW domain (Npw38)
577	1	213	64	702	g3114820	3.00E-88	JM26
578	3	145	27	461	g291888	3.00E-58	cathepsin B
578	3	145	27	461	g181178	3.00E-58	lysosomal proteinase cathepsin B
578	3	145	27	461	g16307393	3.00E-58	cathepsin B

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
579	1	217	1	651	g4588906	7.00E-97	ribosomal protein S7
579	1	217	1	651	g14787424	5.00E-94	Ribosomal protein S7
579	1	217	1	651	g4128206	1.00E-82	40S ribosome protein S7
580	3	212	3	638	g16553223	2.00E-77	unnamed protein product
580	3	212	3	638	g16550444	2.00E-49	unnamed protein product
580	3	212	3	638	g16551429	3.00E-27	unnamed protein product
581	2	190	833	1402	g12841311	2.00E-90	data source:SPTR, source key:Q9WTR7, evidence: ISS-homolog to SIGNAL
581	2	190	833	1402	g16307229	3.00E-90	PEPTIDASE 21 KDA SUBUNIT-putative
581	2	190	833	1402	g13182747	3.00E-90	Unknown (protein for MGC:9299)
582	3	343	387	1415	g11094293	0	microsomal signal peptidase subunit
582	3	343	387	1415	g11094311	0	brain link protein-1
582	3	343	387	1415	g11094297	0	brain link protein-1
583	1	501	247	1749	g10434596	0	brain link protein-1
583	1	501	247	1749	g15929209	0	unnamed protein product
583	1	501	247	1749	g10434367	0	hypothetical protein FLJ12707
584	1	119	217	573	g6249687	1.00E-59	unnamed protein product
584	1	119	217	573	g7243243	1.00E-21	R31155_1
584	1	119	217	573	g16550359	4.00E-21	KIAA1431 protein
586	3	461	63	1445	g14585869	0	unnamed protein product
586	3	461	63	1445	g14042915	0	hypothetical protein SB146
586	3	461	63	1445	g14328009	1.00E-172	unnamed protein product
587	2	572	419	2134	g14915787	0	Unknown (protein for IMAGE:3942111)
587	2	572	419	2134	g16550684	0	WAC
587	2	572	419	2134	g13279044	0	unnamed protein product
588	1	287	1	861	g13274611	1.00E-169	hypothetical protein PRO1741
588	1	287	1	861	g12803253	1.00E-169	glutamate rich WD repeat protein
588	1	287	1	861	g14198122	1.00E-159	Similar to CG12792 gene product
589	2	485	248	1702	g9187612	0	Similar to glutamate rich WD repeat protein GRWD
589	2	485	248	1702	g10436076	0	hypothetical protein, similar to (AF091072.1) predicted protein
589	2	485	248	1702	g14602971	0	unnamed protein product
590	3	405	54	1268	g3540177	0	Unknown (protein for MGC:14981)
							F23269_2

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SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
590	3	405	54	1268	g5080758	1.00E-174	BC331191_1
590	3	405	54	1268	g12855931	1.00E-111	data source:SPTR, source key:P16374, evidence:ISS-putative~similar to ZINC FINGER PROTEIN 60 (ZFP-60) (ZINC FINGER PROTEIN MFG-3)
591	2	172	2	517	g7959207	7.00E-50	KIAA1473 protein
591	2	172	2	517	g16041769	2.00E-48	Unknown (protein for MGC:23189)
591	2	172	2	517	g4235144	5.00E-47	BC39498_1
592	2	728	2	2185	g12052983	0	hypothetical protein
592	2	728	2	2185	g4519270	0	Kruppel-type zinc finger protein
592	2	728	2	2185	g6467206	0	gonadotropin inducible transcription repressor-4
593	1	583	1	1749	g5231271	0	autoimmune enteropathy-related antigen AIE-75
593	1	583	1	1749	g3170200	0	antigen NY-CO-38
593	1	583	1	1749	g16359185	0	Similar to PDZ-73 protein
594	2	375	2	1126	g15823640	4.00E-79	Als2
594	2	375	2	1126	g15823636	8.00E-79	long form
594	2	375	2	1126	g10047191	8.00E-79	KIAA1563 protein
595	3	349	18	1064	g3417297	0	Unknown gene product
595	3	349	18	1064	g16552168	0	unnamed protein product
595	3	349	18	1064	g15559282	5.00E-98	Unknown (protein for MGC:20208)
596	2	94	143	424	g16550359	7.00E-40	unnamed protein product
596	2	94	143	424	g7243243	1.00E-31	KIAA1431 protein
596	2	94	143	424	g4567178	2.00E-29	R31665_2
597	2	390	80	1249	g14042550	1.00E-108	unnamed protein product
597	2	390	80	1249	g13937909	1.00E-108	Similar to KIAA0961 protein
597	2	390	80	1249	g16552245	3.00E-95	unnamed protein product
598	3	467	42	1442	g12804493	0	Unknown (protein for MGC:2615)
598	3	467	42	1442	g18128717	0	unnamed protein product
598	3	467	42	1442	g16549529	0	unnamed protein product
599	3	351	3	1055	g18652252	1.00E-167	target of myb1-like protein 2
599	3	351	3	1055	g3256185	1.00E-121	dJ510H16.1 (target of myb1 (chicken) homolog)
599	3	351	3	1055	g3319953	1.00E-121	TOM1
600	1	535	1	1605	g13676443	1.00E-117	hypothetical protein
600	1	535	1	1605	g6808105	5.00E-91	hypothetical protein

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
600	1	535	1	1605	g18146831	4.00E-86	RGL1
602	3	184	234	785	g12314195	4.00E-74	bA255A11.3 (novel protein similar to KIAA1074)
602	3	184	234	785	g12314164	1.00E-73	bA526D8.2 (novel protein similar to KIAA1074)
602	3	184	234	785	g12053099	3.00E-56	hypothetical protein
603	2	387	131	1291	g16550359	0	unnamed protein product
603	2	387	131	1291	g16550064	1.00E-142	unnamed protein product
603	2	387	131	1291	g13560888	1.00E-120	EZFT-related protein 1
604	1	195	31	615	g14794726	9.00E-95	CUB and sushi multiple domains 1 protein
604	1	195	31	615	g14787181	9.00E-95	CUB and sushi multiple domains protein 1 short form
604	1	195	31	615	g15620839	9.00E-95	KIAA1890 protein
605	3	484	3	1454	g13160492	0	UBX domain-containing protein 1
605	3	484	3	1454	g13160494	0	UBX domain-containing protein 1
605	3	484	3	1454	g14249831	0	UBX domain-containing 2
606	3	118	3	356	g16549907	2.00E-41	unnamed protein product
606	3	118	3	356	g2887445	2.00E-24	KIAA0412
606	3	118	3	356	g3289985	2.00E-24	KIAA0412
607	3	158	453	926	g4185943	5.00E-73	pol protein
607	3	158	453	926	g5802821	7.00E-72	Gag-Pro-Pol protein
607	3	158	453	926	g4456990	7.00E-72	polymerase
608	3	630	3	1892	g499204	1.00E-75	D-E-A-D box protein
608	3	630	3	1892	g4972732	1.00E-75	unknown
608	3	630	3	1892	g7294064	1.00E-75	Dbp73D gene product
609	3	268	756	1559	g12314164	1.00E-151	bA526D8.2 (novel protein similar to KIAA1074)
609	3	268	756	1559	g12314195	1.00E-134	bA255A11.3 (novel protein similar to KIAA1074)
609	3	268	756	1559	g12053099	3.00E-96	hypothetical protein
610	1	372	13	1128	g12842288	1.00E-166	Ank repeat containing protein~data source: Pfam, source key: PF00023, evidence: ISS~putative
610	1	372	13	1128	g7303380	3.00E-21	CG13320 gene product
610	1	372	13	1128	g7293339	6.00E-10	f gene product
612	2	132	203	598	g17016967	2.00E-67	NUANCE
612	2	132	203	598	g17016965	2.00E-67	NUANCE-N-33
612	2	132	203	598	g17016969	2.00E-59	NUANCE

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SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
613	2	617	608	2458	g6634023	0	KIAA0356 protein
613	2	617	608	2458	g7899288	0	unnamed protein product
613	2	617	608	2458	g9367856	1.00E-172	hypothetical protein KIAA0356
614	3	211	93	725	g4314340	1.00E-103	Human alpha-adaptin A homolog
614	3	211	93	725	g15963476	1.00E-103	alpha-adaptin A related protein
614	3	211	93	725	g49878	4.00E-95	alpha-adaptin (A) (AA 1-977)
615	3	487	762	2222	g14042035	0	unnamed protein product
615	3	487	762	2222	g6063139	6.00E-41	BTB/POZ domain zinc finger factor HOF-L
615	3	487	762	2222	g4886505	6.00E-41	hypothetical protein
616	2	972	2	2917	g18314381	0	Similar to mitotic control protein dis3 homolog
616	2	972	2	2917	g15559519	0	Unknown (protein for IMAGE:4561365)
616	2	972	2	2917	g17225572	1.00E-154	KIAA1008 protein
617	3	100	183	482	g18650590	3.00E-34	archaease
617	3	100	183	482	g12841926	3.00E-34	data source:SPTR, source key:Q9VD92, evidence:ISS-putative--related to CG6353 PROTEIN
617	3	100	183	482	g12840887	3.00E-34	data source:SPTR, source key:Q9VD92, evidence:ISS-putative--related to CG6353 PROTEIN
618	1	438	106	1419	g2689446	0	R27945_1
618	1	438	106	1419	g16549907	1.00E-144	unnamed protein product
618	1	438	106	1419	g3289985	1.00E-138	KIAA0412
619	2	138	2870	3283	g5262325	1.00E-43	C35887.1 (ubiquitin-conjugating enzyme E2l (homologous to yeast UBC9))
619	2	138	2870	3283	g4079643	1.00E-43	ubiquitin-conjugating enzyme UbcE2A
619	2	138	2870	3283	g2597931	1.00E-43	ubiquitin-conjugating enzyme, UBC9
620	1	329	1	987	g17105197	1.00E-173	kelch-like protein KLHL6
620	1	329	1	987	g18044145	7.00E-50	Unknown (protein for MGC:28950)
620	1	329	1	987	g12314036	7.00E-50	dJ383J4.1 (A Kelch motif-containing protein)
621	1	380	73	1212	g14575679	0	hemocentin
621	1	380	73	1212	g16551710	0	unnamed protein product
621	1	380	73	1212	g11544425	1.00E-170	bG153O3.1 (similar to C.elegans hemocentin precursor)
622	3	232	366	1061	g7019945	1.00E-117	unnamed protein product
622	3	232	366	1061	g12804721	2.00E-50	Unknown (protein for MGC:2663)
622	3	232	366	1061	g7959207	2.00E-46	KIAA1473 protein

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
623	1	136	115	522	g407466	4.00E-34	QM protein
623	1	136	115	522	g402827	4.00E-34	QM
623	1	136	115	522	g190814	4.00E-34	Wilm's tumor-related protein
624	1	838	37	2550	g6331377	0	KIAA1285 protein
624	1	838	37	2550	g18614026	1.00E-108	zinc finger DNA binding protein p71
624	1	838	37	2550	g5630080	1.00E-106	similar to HUB1; similar to BAA24380 (PID:g2789430)
625	3	255	3	767	g18027350	1.00E-148	unknown
625	3	255	3	767	g15072406	1.00E-147	TNFAIP1-like protein
625	3	255	3	767	g16152040	1.00E-145	polymerase delta-interacting protein 1
626	2	327	2	982	g13277864	1.00E-161	Similar to ATPase, H+ transporting, lysosomal (vacuolar proton pump) 42kD
626	2	327	2	982	g15082451	1.00E-153	Unknown (protein for MGC:20253)
626	2	327	2	982	g37643	4.00E-93	vacuolar proton-ATPase
627	2	264	11	802	g1208742	1.00E-137	protein B
627	2	264	11	802	g1200503	1.00E-137	B
627	2	264	11	802	g16878002	1.00E-137	Unknown (protein for MGC:12569)
628	3	163	1377	1865	g16549383	6.00E-75	unnamed protein product
628	3	163	1377	1865	g15824463	2.00E-57	DiGeorge syndrome-related protein FKSG4
628	3	163	1377	1865	g3094014	2.00E-56	unknown
629	1	262	1	786	g14043223	2.00E-95	Unknown (protein for MGC:15677)
629	1	262	1	786	g16076870	2.00E-52	LD37206p
629	1	262	1	786	g7297712	3.00E-49	CG6144 gene product
630	3	323	879	1847	g7294748	7.00E-48	CG7616 gene product
630	3	323	879	1847	g12847351	2.00E-30	data source:SPTR, source key:Q9JUE6, evidence:ISS-homolog to HYPOTHETICAL 52.0 KDA PROTEIN-putative RIKEN cDNA 2610005A10 gene
630	3	323	879	1847	g14714781	2.00E-30	NALP4
632	1	175	61	585	g17064172	1.00E-80	unnamed protein product
632	1	175	61	585	g16552162	1.00E-28	unnamed protein product
632	1	175	61	585	g17901636	6.00E-20	Unknown (protein for MGC:19357)
633	1	561	1	1683	g17389275	0	unnamed protein product
633	1	561	1	1683	g15209718	1.00E-173	unnamed protein product
633	1	561	1	1683	g3702269	1.00E-151	sodium iodide symporter
634	3	276	30	857	g3955100	2.00E-75	vacuolar adenosine triphosphatase subunit D



TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
634	3	276	30	857	g15029719	2.00E-75	Unknown (protein for MGC:18332)
634	3	276	30	857	g14250784	2.00E-75	Unknown (protein for MGC:15351)
635	1	398	490	1683	g3712671	1.00E-137	vascular endothelial growth factor
635	1	398	490	1683	g340301	1.00E-133	vascular permeability factor precursor
635	1	398	490	1683	g340215	1.00E-133	vascular endothelial growth factor
636	2	197	689	1279	g17045994	1.00E-101	unnamed protein product
636	2	197	689	1279	g36615	1.00E-82	serine/threonine protein kinase
636	2	197	689	1279	g7297009	8.00E-72	CG7236 gene product
637	3	307	3	923	g15488871	1.00E-172	aquaporin 3
637	3	307	3	923	g1854374	1.00E-172	aquaporin 3
637	3	307	3	923	g4416299	1.00E-164	aquaporin-3; AQP3
638	3	263	708	1496	g16549180	1.00E-102	unnamed protein product
638	3	263	708	1496	g5441615	1.00E-101	zinc finger protein
638	3	263	708	1496	g488555	1.00E-99	zinc finger protein ZNF135
639	1	673	241	2259	g5080758	0	BC331191_1
639	1	673	241	2259	g1769491	0	kruppel-related zinc finger protein
639	1	673	241	2259	g3135968	0	b3418.1 (zinc finger protein 184 (Kruppel-like))
640	3	198	66	659	g12805201	3.00E-17	Similar to zinc finger protein 97
640	3	198	66	659	g14042682	3.00E-15	unnamed protein product
640	3	198	66	659	g5453423	3.00E-13	epstein-barr virus-induced zinc finger protein
641	1	947	34	2874	g6329952	0	KIAA1141 protein
641	1	947	34	2874	g17391340	0	Unknown (protein for MGC:20009)
641	1	947	34	2874	g17981470	0	zinc finger protein ZFP100
642	3	285	318	1172	g15489325	1.00E-163	Similar to hypothetical protein MGC10520
642	3	285	318	1172	g16549189	1.00E-110	unnamed protein product
642	3	285	318	1172	g488555	1.00E-107	zinc finger protein ZNF135
643	1	2044	16	6147	g30186	0	CR1 precursor protein
643	1	2044	16	6147	g306680	0	complement receptor 1
643	1	2044	16	6147	g557725	0	complement receptor 1
644	3	827	60	2540	g1235672	0	metalloprotease/disintegrin/cysteine-rich protein precursor
644	3	827	60	2540	g6630618	0	KIAA0021 protein
644	3	827	60	2540	g1235676	0	metalloprotease/disintegrin/cysteine rich protein precursor

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
645	2	378	821	1954	g14134965	0	unnamed protein product
645	2	378	821	1954	g219867	6.00E-57	HM74
645	2	378	821	1954	g11558406	8.00E-57	putative seven transmembrane spanning receptor
646	2	263	2	790	g15277259	1.00E-157	zinc finger protein homologous to mouse Zfp91
646	2	263	2	790	g15865601	1.00E-157	FKSG11
646	2	263	2	790	g453376	1.00E-154	zinc finger protein PFZ
647	1	256	856	1623	g13436164	1.00E-152	carbonic anhydrase III, muscle specific
647	1	256	856	1623	g179789	1.00E-152	carbonic anhydrase III
647	1	256	856	1623	g15029812	1.00E-140	carbonic anhydrase 3
648	1	359	1	1077	g512464	0	u-PA receptor
648	1	359	1	1077	g4335703	0	UPAR_HUMAN; GPI-ANCHORED FORM PRECURSOR; U-PAR; MONOCYTE ACTIVATION ANTIGEN MO3; CD87 ANTIGEN
648	1	359	1	1077	g37605	0	urokinase plasminogen activator receptor
649	2	727	233	2413	g5006263	0	organic anion transporter OATP-B
649	2	727	233	2413	g4240249	0	KIAA0880 protein
649	2	727	233	2413	g11990589	0	organic anion transporter polypeptide-related protein 2
650	3	93	909	1187	g54912	2.00E-43	tropomyosin 5
650	3	93	909	1187	g438878	2.00E-43	tropomyosin
650	3	93	909	1187	g312928	2.00E-43	tropomyosin isoform 6
651	2	374	185	1306	g13365855	0	hypothetical protein
651	2	374	185	1306	g2072425	1.00E-70	non-lens beta gamma-crystallin like protein
651	2	374	185	1306	g15207879	1.00E-65	hypothetical protein
652	1	233	592	1290	g33967	1.00E-124	interferon regulatory factor-2 (AA 1-349)
652	1	233	592	1290	g16041826	1.00E-124	interferon regulatory factor 2
652	1	233	592	1290	g6090306	1.00E-116	unnamed protein product
653	1	564	1	1692	g6733355	0	unnamed protein product
653	1	564	1	1692	g2967646	0	Smad2
653	1	564	1	1692	g2695663	0	MAD-related protein Smad2
654	2	499	299	1795	g1289371	0	Ikaros/LyF-1 homolog
654	2	499	299	1795	g1911483	0	hik1
654	2	499	299	1795	g2330595	0	Ikaros transcription factor
655	1	1968	481	6384	g3413888	0	KIAA0463 protein

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
655	1	1968	481	6384	g1655432	0	plexin 2
655	1	1968	481	6384	g6010215	0	OCT/plexin-A2 protein
656	2	321	458	1420	g18480242	1.00E-152	olfactory receptor MOR138-2
656	2	321	458	1420	g15293713	1.00E-123	olfactory receptor
656	2	321	458	1420	g18480166	1.00E-106	olfactory receptor MOR138-1
657	1	415	493	1737	g1197538	0	myocyte-specific enhancer factor 2A, C4 form
657	1	415	493	1737	g34536	0	myocyte-specific enhancer factor 2 (MEF2)
657	1	415	493	1737	g432656	0	serum response factor-related protein
658	2	578	905	2638	g14009457	0	protocadherin-beta12
658	2	578	905	2638	g5457031	0	protocadherin beta 12
658	2	578	905	2638	g5457029	0	protocadherin beta 11
659	2	449	1112	2458	g32033	0	put. HBK2 protein (AA 1-529)
659	2	449	1112	2458	g57667	0	put. RCK2 protein (AA 1-530)
659	2	449	1112	2458	g199893	0	murine potassium channel protein
660	2	206	14	631	g7340874	2.00E-96	ESTs D15590(C0900), D48950(S15542), D22684(C0900) correspond to a region of the predicted gene. ~Similar to Arabidopsis thaliana 60S ribosomal protein L11A (L16A). (P42795)
660	2	206	14	631	g7630065	1.00E-94	ribosomal protein L11-like
660	2	206	14	631	g14517470	1.00E-94	AT4g18730/F28A21_140
661	3	423	36	1304	g17225038	1.00E-173	CaMKK beta 1 isoform
661	3	423	36	1304	g17225036	1.00E-173	CaMKK beta 1 isoform
661	3	423	36	1304	g14522878	1.00E-173	calcium/calmodulin-dependent protein kinase b2
662	3	446	693	2030	g4096339	0	zinc finger protein
662	3	446	693	2030	g6691968	1.00E-168	dJ148M19.1 (zinc finger protein)
662	3	446	693	2030	g5457352	2.00E-78	AP-2rep protein
663	3	842	3	2528	g2343289	0	NMDAR1 subunit isoform 4b
663	3	842	3	2528	g2343287	0	NMDAR1 subunit isoform 3b
663	3	842	3	2528	g56765	0	NMDA receptor subunit, type NMDAR1-LL
664	2	184	2	553	g2668738	2.00E-89	translation initiation factor 5A
664	2	184	2	553	g1546919	2.00E-89	translation initiation factor 5A
664	2	184	2	553	g3789948	2.00E-83	translation initiation factor 5A
665	3	267	903	1703	g14139788	1.00E-154	unnamed protein product

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
665	3	267	903	1703	g12405805	1.00E-154	unnamed protein product
665	3	267	903	1703	g6453491	1.00E-154	hypothetical protein
666	2	298	5	898	g13879442	1.00E-119	Similar to RIKEN cDNA 2310035M22 gene
666	2	298	5	898	g12855490	1.00E-114	data source:SPTR, source key:P24390, evidence:ISS-homolog to ER LUMEN PROTEIN RETAINING RECEPTOR 1 (KDEL RECEPTOR 1)-putative
666	2	298	5	898	g12848905	1.00E-111	data source:SPTR, source key:O60858, evidence:ISS-homolog to LEUKEMIA ASSOCIATED PROTEIN 5 (B-CELL CHRONIC LYMPHOCTIC LEUKEMIA TUMOR SUPPRESSOR LEU5)-putative
667	2	232	128	823	g1763638	1.00E-111	alpha1A-voltage-dependent calcium channel
667	2	232	128	823	g1763636	1.00E-111	alpha1A-voltage-dependent calcium channel
667	2	232	128	823	g1763632	1.00E-111	alpha1A-voltage-sensitive calcium channel
668	2	154	206	667	g12837586	1.00E-64	data source:SPTR, source key:P37545, evidence:ISS-putative-related to HYPOTHETICAL 29.2 KDA PROTEIN IN METS-KSGA INTERGENIC REGION
668	2	154	206	667	g2632306	5.00E-13	similar to hypothetical proteins
668	2	154	206	667	g467428	5.00E-13	unknown
669	1	287	1	861	g14042544	1.00E-158	unnamed protein product
669	1	287	1	861	g7650202	1.00E-151	CECR1 protein
669	1	287	1	861	g17646182	1.00E-116	CECR1
670	3	538	195	1808	g16307285	0	Unknown (protein for IMAGE:3877337)
670	3	538	195	1808	g15208051	1.00E-157	hypothetical protein
670	3	538	195	1808	g12855904	8.00E-96	evidence:NAS-hypothetical protein-putative
671	1	474	2767	4188	g10434329	0	unnamed protein product
671	1	474	2767	4188	g14133251	0	KIAA1479 protein
671	1	474	2767	4188	g10434456	0	unnamed protein product
672	3	424	501	1772	g4589566	0	KIAA0961 protein
672	3	424	501	1772	g13676461	0	hypothetical protein
672	3	424	501	1772	g456269	0	zinc finger protein 30
673	2	425	155	1429	g5262574	0	hypothetical protein
673	2	425	155	1429	g17861380	0	nesprin-2 beta
673	2	425	155	1429	g17016967	0	NUANCE
674	3	514	3	1544	g17049366	0	unnamed protein product
674	3	514	3	1544	g13447749	0	fibroblast growth factor receptor 5

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
674	3	514	3	1544	g10944887	0	FGFR-like protein
675	1	149	145	591	g7959207	2.00E-26	KIAA1473 protein
675	1	149	145	591	g498736	4.00E-26	zinc finger protein
675	1	149	145	591	g16551398	6.00E-26	unnamed protein product
676	2	347	134	1174	g13938261	4.00E-91	Unknown (protein for MGC:15514)
676	2	347	134	1174	g5262557	4.00E-91	hypothetical protein
676	2	347	134	1174	g15488954	1.00E-89	Unknown (protein for MGC:8872)
677	3	552	3	1658	g12803309	0	hypothetical protein FLJ20481
677	3	552	3	1658	g7020611	0	unnamed protein product
677	3	552	3	1658	g12853070	0	EF hand containing protein~data source:Pfam, source key:PF00036, evidence:ISS~putative
678	1	488	1	1464	g14794726	0	CUB and sushi multiple domains 1 protein
678	1	488	1	1464	g14787176	0	CSMD1
678	1	488	1	1464	g15620827	1.00E-172	KIAA1884 protein
679	1	398	4	1197	g16549477	0	unnamed protein product
679	1	398	4	1197	g12214288	5.00E-87	dJ402H5.2 (novel protein similar to worm and fly proteins)
679	1	398	4	1197	g7302178	5.00E-27	CG11212 gene product
680	1	613	103	1941	g3643115	0	protein inhibitor of activated STAT protein PIASx-beta
680	1	613	103	1941	g13542785	0	Unknown (protein for MGC:11445)
680	1	613	103	1941	g3643113	0	protein inhibitor of activated STAT protein PIASx-alpha
681	1	420	1	1260	g12853497	0	BTB/POZ domain containing protein~data source:Pfam, source key:PF00651, evidence:ISS~putative
681	1	420	1	1260	g18204103	0	RIKEN cDNA 4930429H24 gene
681	1	420	1	1260	g7019911	0	unnamed protein product
682	1	287	1	861	g18027414	1.00E-111	unknown
682	1	287	1	861	g13358646	1.00E-96	hypothetical protein
682	1	287	1	861	g12843142	3.00E-91	TPR Domain containing protein~data source:Pfam, source key:PF00515, evidence:ISS~putative
683	3	428	621	1904	g12309630	0	bA438823.1 (neuronal leucine-rich repeat protein)
683	3	428	621	1904	g16551759	0	unnamed protein product
683	3	428	621	1904	g15029689	1.00E-122	Unknown (protein for MGC:17422)
684	1	809	25	2451	g6633952	0	KIAA0137 protein

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
684	1	809	25	2451	g2217933	0	PKU-beta
684	1	809	25	2451	g6063017	0	tousled-like kinase 1
685	3	543	234	1862	g12836718	0	data source:SPTR, source key:Q918M2, evidence:ISS~putative~related to PUTATIVE N-TERMINAL ACETYLTRANSFERASE
685	3	543	234	1862	g13195460	0	putative acetyltransferase
685	3	543	234	1862	g14589342	0	putative N-acetyltransferase
686	3	442	3	1328	g12856025	0	WD domain, G-beta repeat containing protein~data source:Pfam, source key:PF00400, evidence:ISS~putative
686	3	442	3	1328	g12846941	1.00E-107	WD domain, G-beta repeat containing protein~data source:Pfam, source key:PF00400, evidence:ISS~putative
686	3	442	3	1328	g17488592	1.00E-107	unknown protein
687	3	502	126	1631	g10800564	0	bA338L11.1 (novel CUB domain protein similar to attractin)
687	3	502	126	1631	g8118082	1.00E-137	membrane attractin precursor
687	3	502	126	1631	g8118083	1.00E-137	secreted attractin precursor
688	3	316	3	950	g18480302	1.00E-111	olfactory receptor MOR262-10
688	3	316	3	950	g5869927	1.00E-104	olfactory receptor
688	3	316	3	950	g8919698	1.00E-104	olfactory receptor
689	1	265	1	795	g12846015	1.00E-153	data source:SPTR, source key:Q9NZ01, evidence:ISS~homolog to SYNAPTIC GLYCOPROTEIN SC2 (UNKNOWN) (PROTEIN FOR MGC:14589) (SIMILAR TO CG10849 GENE PRODUCT)-putative
689	1	265	1	795	g256994	1.00E-150	SC2
689	1	265	1	795	g18044806	1.00E-150	RIKEN cDNA A230102P12 gene
690	2	182	905	1450	g6015476	4.00E-60	C-terminal binding protein 2
690	2	182	905	1450	g15426462	4.00E-60	Unknown (protein for MGC:13751)
690	2	182	905	1450	g12034656	4.00E-60	ribeye
691	2	613	119	1957	g15020827	0	dJ29K1.2 (KIAA0426 (C2H2 type zinc finger protein))
691	2	613	119	1957	g2887427	0	KIAA0426
691	2	613	119	1957	g4097501	0	zinc finger protein 96
692	1	978	337	3270	g14602998	0	Unknown (protein for IMAGE:4121355)
692	1	978	337	3270	g1657837	0	p116Rip
692	1	978	337	3270	g10803059	0	p116RIP

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
693	2	538	2	1615	g11323324	0	dJ138B7.3.2 (lethal (3) malignant brain tumor ((3)mbt) protein (Drosophila) homolog (isoform 2) (KIAA0681))
693	2	538	2	1615	g3327176	0	KIAA0681 protein
693	2	538	2	1615	g11323323	0	dJ138B7.3.1 (Continued from dJ862K6.1 In Em:AL031681)
694	3	414	669	1910	g7960216	0	RACK-like protein PRKCBP1
694	3	414	669	1910	g11385648	0	CTCL tumor antigen se14-3
694	3	414	669	1910	g17980969	0	se14-3r protein
695	2	503	1157	2665	g7242977	0	KIAA1311 protein
695	2	503	1157	2665	g14042145	1.00E-113	unnamed protein product
695	2	503	1157	2665	g14041949	1.00E-112	unnamed protein product
696	2	1270	224	4033	g11596412	0	GAC-1
696	2	1270	224	4033	g10437204	0	unnamed protein product
696	2	1270	224	4033	g7019901	0	unnamed protein product
697	2	349	2	1048	g6599275	1.00E-111	hypothetical protein
697	2	349	2	1048	g5805208	1.00E-111	fas-associated factor 1
697	2	349	2	1048	g4680647	1.00E-111	CGI-03 protein
699	1	150	982	1431	g16603814	2.00E-75	small GTP-binding protein
699	1	150	982	1431	g13177778	2.00E-75	SAR1 protein
699	1	150	982	1431	g12052967	2.00E-75	hypothetical protein
700	3	664	204	2195	g7959343	1.00E-161	KIAA1538 protein
700	3	664	204	2195	g12844361	1.00E-87	BTB/POZ domain containing protein~data source:Pfam, source key:PF00651, evidence:ISS~putative
700	3	664	204	2195	g2085786	4.00E-32	similar to zinc finger 5 protein from Gallus gallus, U51640 (PID:g1399185)
701	3	274	3	824	g10434090	1.00E-142	unnamed protein product
701	3	274	3	824	g12836022	2.00E-53	data source:SPTR, source key:Q9P2N7, evidence:ISS~homolog to HYPOTHETICAL PROTEIN KIAA1309 (FRAGMENT)-putative
701	3	274	3	824	g7243089	7.00E-53	KIAA1354 protein
702	2	281	2	844	g306487	1.00E-130	cap-binding protein
702	2	281	2	844	g15214959	1.00E-129	Similar to eukaryotic translation initiation factor 4E
702	2	281	2	844	g7673694	1.00E-128	translation initiation factor eIF-4E
703	3	210	3	632	g13544026	4.00E-98	putative zinc finger protein from EUROIMAGE 566589

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
703	3	210	3	632	g5102580	4.00E-98	hypothetical protein, similar to (AF134804) putative zinc finger transcription factor OVO1
703	3	210	3	632	g10433647	2.00E-97	unnamed protein product
704	1	625	40	1914	g3256264	0	MTG8-related protein MTG16a
704	1	625	40	1914	g3256266	0	MTG8-related protein MTG16b
704	1	625	40	1914	g2723941	0	ETO/MTG8-related protein ETO-2
705	1	424	76	1347	g2664429	0	hypothetical protein
705	1	424	76	1347	g16549891	0	unnamed protein product
705	1	424	76	1347	g18461369	1.00E-179	hexaribonucleotide binding protein 2
706	3	592	2766	4541	g17223624	0	ATP-binding cassette A9
706	3	592	2766	4541	g4240130	0	KIAA0822 protein
706	3	592	2766	4541	g17223626	0	ATP-binding cassette A10
707	1	661	274	2256	g17017251	0	MEGF12
707	1	661	274	2256	g17386053	0	Jedi protein
707	1	661	274	2256	g18252658	1.00E-116	Jedi-736 protein
708	3	608	252	2075	g6634025	1.00E-172	KIAA0379 protein
708	3	608	252	2075	g6453538	1.00E-160	hypothetical protein
708	3	608	252	2075	g4803678	5.00E-48	ankyrin (brank-2)
709	2	860	266	2845	g10434450	0	unnamed protein product
709	2	860	266	2845	g6002623	0	putative RNA-binding protein Q99
709	2	860	266	2845	g10047199	0	KIAA1567 protein
710	2	1215	2	3646	g7243153	0	KIAA1386 protein
710	2	1215	2	3646	g6807862	0	hypothetical protein
710	2	1215	2	3646	g7022270	0	unnamed protein product
711	2	468	2	1405	g13097657	0	Unknown (protein for IMAGE:3611719)
711	2	468	2	1405	g8885518	0	hypothetical protein
711	2	468	2	1405	g12854661	1.00E-164	Ank repeat containing protein~data source:Pfam, source key:PF00023, evidence:ISS~putative
712	1	738	1	2214	g3327040	0	KIAA0613 protein
712	1	738	1	2214	g11612596	0	cypher1
712	1	738	1	2214	g6969629	0	oracle 1 protein
713	2	565	2	1696	g4126475	0	BAP2-alpha protein



TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
713	2	565	2	1696	g4239984	0	insulin receptor substrate protein of 53 kDa (a shorter form)
713	2	565	2	1696	g15559320	0	Similar to BAI1-associated protein 2
714	1	86	370	627	g12652727	5.00E-44	Unknown (protein for IMAGE:3352566)
714	1	86	370	627	g16552245	5.00E-13	unnamed protein product
714	1	86	370	627	g4567180	1.00E-12	BC37295_2 (partial)
715	3	221	3	665	g12655189	1.00E-117	testin
715	3	221	3	665	g10443903	1.00E-117	TESTIN 3
715	3	221	3	665	g10443902	1.00E-117	TESTIN 2
716	3	330	3	992	g13516831	0	MAIL
716	3	330	3	992	g13442951	1.00E-178	MAIL
716	3	330	3	992	g13702146	1.00E-173	IL-1 inducible nuclear ankyrin-repeat protein
717	2	1036	2	3109	g7243105	1.00E-118	KIAA1362 protein
717	2	1036	2	3109	g7023688	1.00E-109	unnamed protein product
717	2	1036	2	3109	g12855942	1.00E-108	data source:MGD, source key:MGI:1261419, evidence:ISS-ethanol decreased 4-putative
718	3	532	1404	2999	g7020464	1.00E-159	unnamed protein product
718	3	532	1404	2999	g757872	1.00E-150	env
718	3	532	1404	2999	g5802822	1.00E-150	envelope protein
719	1	1373	1	4119	g12240161	0	uveal autoantigen
719	1	1373	1	4119	g12240158	0	uveal autoantigen
719	1	1373	1	4119	g10944718	0	C3VS protein
720	2	280	2	841	g18034491	1.00E-152	SRp35
720	2	280	2	841	g18203864	1.00E-151	Similar to FUS interacting protein (serine-arginine rich) 2
720	2	280	2	841	g3327976	1.00E-63	TLS-associated protein TASR-2
721	2	288	2	865	g16553765	1.00E-134	unnamed protein product
721	2	288	2	865	g12839186	1.00E-128	data source:SPTR, source key:Q9VS60, evidence:ISS-putative-related to CG8576 PROTEIN
721	2	288	2	865	g1072250	1.00E-31	F53B1.2 gene product
722	2	175	200	724	g18645200	9.00E-93	hypothetical gene supported by XM_059671
723	2	385	92	1246	g12803351	1.00E-136	Unknown (protein for IMAGE:3050476)
723	2	385	92	1246	g18204315	1.00E-136	Unknown (protein for MGC:31975)
723	2	385	92	1246	g2352822	2.00E-42	glucose-6-phosphatase

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
724	2	269	284	1090	g16041142	1.00E-133	hypothetical protein
724	2	269	284	1090	g14017813	4.00E-88	KIAA1798 protein
724	2	269	284	1090	g11323323	5.00E-84	dJ138B7.3.1 (Continued from dJ862K6.1 in Em:AL031681)
725	2	552	299	1954	g17064170	0	HSV-1 stimulating-related protein
725	2	552	299	1954	g4240233	0	KIAA0872 protein
725	2	552	299	1954	g14495695	1.00E-114	Unknown (protein for MGC:15935)
726	2	296	8	895	g13435476	1.00E-133	Unknown (protein for MGC:6708)
726	2	296	8	895	g12849125	1.00E-129	DNA segment, Chr 10, University of California at Los Angeles 1~data source:MGD, source key:MGI:88930, evidence:ISS~putative
726	2	296	8	895	g12842006	6.00E-97	DNA segment, Chr 10, University of California at Los Angeles 1~data source:MGD, source key:MGI:88930, evidence:ISS~putative
727	3	462	645	2030	g10047211	0	KIAA1573 protein
727	3	462	645	2030	g14388334	2.00E-85	hypothetical protein
727	3	462	645	2030	g7298275	4.00E-13	BG:DS07473.1 gene product
728	2	126	209	586	g2306773	2.00E-20	zinc finger protein
728	2	126	209	586	g11137801	2.00E-20	dJ265C24.2 (zinc finger protein 192 (LD5-1))
728	2	126	209	586	g1373394	2.00E-20	zinc finger protein
729	1	474	1	1422	g7959207	0	KIAA1473 protein
729	1	474	1	1422	g1017722	0	repressor transcriptional factor
729	1	474	1	1422	g16041769	0	Unknown (protein for MGC:23189)
730	1	241	1	723	g12855389	1.00E-41	data source:SPTR, source key:Q9N5L6, evidence:ISS~putative--related to H23L24.3 PROTEIN
730	1	241	1	723	g15718609	1.00E-40	Hypothetical protein H23L24.3
730	1	241	1	723	g7301565	1.00E-33	CG5987 gene product
731	1	258	70	843	g1199602	1.00E-116	cyclophilin-like protein
731	1	258	70	843	g1199598	1.00E-116	cyclophilin-like protein CyP-60
731	1	258	70	843	g1199600	1.00E-116	cyclophilin-like protein
732	1	161	46	528	g17511871	6.00E-94	Unknown (protein for MGC:32104)
732	1	161	46	528	g14042715	2.00E-68	unnamed protein product
732	1	161	46	528	g7023417	2.00E-68	unnamed protein product
733	3	456	3	1370	g16306806	0	zinc finger protein 43 (HTF6)
733	3	456	3	1370	g38032	0	ZNF43

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
733	3	456	3	1370	g186774	0	zinc finger protein
734	2	454	2	1363	g14042850	1.00E-117	unnamed protein product
734	2	454	2	1363	g12052983	6.00E-85	hypothetical protein
734	2	454	2	1363	g487785	6.00E-76	zinc finger protein ZNF136
735	2	153	2	460	g37910	1.00E-59	precursor
735	2	153	2	460	g17511825	5.00E-59	Similar to immunoglobulin kappa constant
735	2	153	2	460	g560842	1.00E-58	anti-Sm antibody VL chain (V kappa 4/J kappa 3)
736	1	319	235	1191	g6808105	9.00E-80	hypothetical protein
736	1	319	235	1191	g13676443	3.00E-79	hypothetical protein
736	1	319	235	1191	g18146831	9.00E-63	RGL1
737	1	245	433	1167	g18034086	1.00E-133	ankyrin repeat domain-containing SOCS box protein Asb-15
737	1	245	433	1167	g18034106	1.00E-125	ankyrin repeat domain-containing SOCS box protein Asb-15
737	1	245	433	1167	g15451412	1.00E-105	hypothetical protein
738	2	432	2	1297	g5050962	4.00E-19	dJ34821.5 (PUTATIVE novel protein with ZU5 domain similar to part of Tight Junction Protein ZO1 (TJP1) and UNC5 Homologs)
738	2	432	2	1297	g2088527	7.00E-17	rostral cerebellar malformation protein
738	2	432	2	1297	g2055394	5.00E-15	transmembrane receptor UNC5H2
739	1	1206	40	3657	g7297900	1.00E-132	CG6734 gene product
739	1	1206	40	3657	g3880102	6.00E-25	contains similarity to Pfam domain: PF00400 (WD domain, G-beta repeat), Score=38.1, E-value=6.5e-08, N=3; PF01363 (FYVE zinc finger), Score=115.4, E-value=1.3e-31, N=1; PF02138 (Beige/BEACH domain), Score=773.7, E-value=2.4e-229, N=1 -cDNA EST yk136h12.5 comes from this gene-cDNA EST yk265b4.5 comes from this gene-cDNA EST yk319c2.5 comes from this gene-cDNA EST yk359g9.5 comes from this gene-cDNA EST yk635c4.5 comes from this gene-cDNA EST yk193g4.5 comes from this gene-cDNA EST yk342c8.5 comes from this gene-cDNA EST yk356b1.5 comes from this gene-cDNA EST yk399d2.5 comes from this gene

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
739	1	1206	40	3657	g3880448	6.00E-25	contains similarity to Pfam domain: PF00400 (WD domain, G-beta repeat), Score=38.1, E-value=6.5e-08, N=3; PF01363 (FVE zinc finger), Score=115.4, E-value=1.3e-31, N=1; PF02138 (Beige/BEACH domain), Score=773.7, E-value=2.4e-229, N=1~cDNA EST yk136h12.5 comes from this gene~cDNA EST yk265b4.5 comes from this gene~cDNA EST yk319c2.5 comes from this gene~cDNA EST yk359g9.5 comes from this gene~cDNA EST yk635c4.5 comes from this gene~cDNA EST yk193g4.5 comes from this gene~cDNA EST yk342c8.5 comes from this gene~cDNA EST yk356b1.5 comes from this gene~cDNA EST yk399d2.5 comes from this gene
741	3	115	447	791	g5080758	8.00E-17	BC331191_1
741	3	115	447	791	g10047183	2.00E-13	KIAA1559 protein
741	3	115	447	791	g15021881	3.00E-13	hypothetical protein
742	2	215	2	646	g14279194	1.00E-109	aldo-keto reductase loopADR
742	2	215	2	646	g12804019	1.00E-109	Similar to aldo-keto reductase
742	2	215	2	646	g15215178	1.00E-68	RIKEN cDNA 1810061110 gene
743	1	290	166	1035	g16551783	1.00E-115	unnamed protein product
743	1	290	166	1035	g881564	8.00E-46	ZNF157
743	1	290	166	1035	g14456632	1.00E-62	dJ54B20.6 (zinc finger protein 81 (HFZ20))
744	3	519	3	1559	g15559662	0	Unknown (protein for MGC:20975)
744	3	519	3	1559	g16877077	0	Unknown (protein for MGC:24494)
744	3	519	3	1559	g9886891	4.00E-45	zinc finger protein 276 C2H2 type
745	1	514	1	1542	g16552010	0	unnamed protein product
745	1	514	1	1542	g12836633	1.00E-120	data source:Pfam, source key:PF00093, evidence:ISS~putative~von Willebrand factor type C domain containing protein
745	1	514	1	1542	g7768636	1.00E-54	Klelln
746	1	63	157	345	g347906	4.00E-18	zinc finger protein
746	1	63	157	345	g13435780	3.00E-16	Similar to Kruppel associated box (KRAB) zinc finger 1
746	1	63	157	345	g5823276	5.00E-16	Kruppel-like protein
748	3	168	399	902	g11611571	2.00E-54	hypothetical protein
748	3	168	399	902	g9886891	2.00E-52	zinc finger protein 276 C2H2 type
748	3	168	399	902	g16877077	9.00E-19	Unknown (protein for MGC:24494)
749	1	694	1	2082	g13936547	0	formin-binding protein 17

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
749	1	694	1	2082	g3043632	0	KIAA0554 protein
749	1	694	1	2082	g10435680	0	unnamed protein product
751	3	448	453	1796	g58491	0	E1b 55k protein (transformation)
751	3	448	453	1796	g209820	0	transformation-associated protein
751	3	448	453	1796	g17105043	1.00E-163	54.7 kDa
752	3	800	387	2786	g992893	0	phosphoinositol 3-phosphate binding protein-1
752	3	800	387	2786	g18204000	0	Similar to pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member 4
752	3	800	387	2786	g10045840	1.00E-33	TPC2
753	1	846	1	2538	g6329945	0	KIAA1140 protein
753	1	846	1	2538	g4972746	1.00E-146	unknown
753	1	846	1	2538	g7302173	1.00E-146	BcDNA:LD21719 gene product
754	1	117	217	567	g16550444	4.00E-28	unnamed protein product
754	1	117	217	567	g12652759	7.00E-27	hypothetical protein FLJ20557
754	1	117	217	567	g7020745	7.00E-27	unnamed protein product
755	1	211	1	633	g487284	1.00E-131	CRP2 (cysteine-rich protein 2)
755	1	211	1	633	g12805265	1.00E-130	cysteine-rich protein 2
755	1	211	1	633	g12805261	1.00E-130	cysteine-rich protein 2
756	3	386	630	1787	g12052983	1.00E-176	hypothetical protein
756	3	386	630	1787	g5262560	1.00E-124	hypothetical protein
756	3	386	630	1787	g10434856	1.00E-118	unnamed protein product
757	1	237	1	711	g17105197	1.00E-120	kelch-like protein KLHL6
757	1	237	1	711	g10439155	3.00E-36	unnamed protein product
757	1	237	1	711	g6329805	6.00E-31	KIAA1129 protein
758	2	972	2	2917	g18314381	0	Similar to mitotic control protein dis3 homolog
758	2	972	2	2917	g15559519	0	Unknown (protein for IMAGE:4561365)
758	2	972	2	2917	g17225572	1.00E-154	KIAA1008 protein
759	1	313	1	939	g206734	1.00E-173	ribosomal protein L5
759	1	313	1	939	g57125	1.00E-171	ribosomal protein L5 (AA 1-297)
759	1	313	1	939	g12850263	1.00E-171	data source:MGI, source key:MGI:102854, evidence:ISS-putative-ribosomal protein L5
760	3	217	1614	2264	g3327090	1.00E-118	KIAA0638 protein

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
760	3	217	1614	2264	g14042238	1.00E-109	unnamed protein product
760	3	217	1614	2264	g15991879	1.00E-109	Unknown (protein for MGC:4704)
761	3	229	3	689	g12314195	1.00E-121	bA255A11.3 (novel protein similar to KIAA1074)
761	3	229	3	689	g12314164	3.00E-97	bA526D8.2 (novel protein similar to KIAA1074)
761	3	229	3	689	g12053099	2.00E-71	hypothetical protein
762	1	594	958	2739	g7959265	0	KIAA1502 protein
762	1	594	958	2739	g14035822	0	unnamed protein product
762	1	594	958	2739	g5764665	0	cerebral cell adhesion molecule
763	1	689	364	2430	g13623407	0	Similar to RIKEN cDNA 2810468K17 gene
763	1	689	364	2430	g14495695	0	Unknown (protein for MGC:15935)
763	1	689	364	2430	g13874543	0	hypothetical protein
764	2	248	743	1486	g2997747	4.00E-29	tetraspan TM4SF; Tspan-4
764	2	248	743	1486	g17939510	4.00E-29	transmembrane 4 superfamily member 7
764	2	248	743	1486	g12653241	4.00E-29	transmembrane 4 superfamily member 7
765	1	304	91	1002	g12232324	1.00E-161	hUPF3B
765	1	304	91	1002	g12620408	1.00E-158	UPF3X
765	1	304	91	1002	g12860428	6.00E-76	data source:SPTR, source key:Q9H1J0, evidence:ISS~homolog to HUPF3B~putative
766	1	128	439	822	g12856090	7.00E-62	data source:SPTR, source key:Q9Z2B2, evidence:ISS~putative~similar to BRAIN MITOCHONDRIAL CARRIER PROTEIN-1 (BMCP-1)
766	1	128	439	822	g12854104	7.00E-62	data source:SPTR, source key:Q9Z2B2, evidence:ISS~putative~similar to BRAIN MITOCHONDRIAL CARRIER PROTEIN-1 (BMCP-1)
766	1	128	439	822	g4678718	5.00E-51	dJ2013.1 (brain mitochondrial carrier protein-1 (BMCP1))
767	1	378	139	1272	g508729	0	thymopoietin gamma
767	1	378	139	1272	g3283900	0	thymopoietin gamma
767	1	378	139	1272	g1335847	1.00E-177	thymopoietin gamma
768	2	358	218	1291	g18204012	0	Similar to RIKEN cDNA B830026H24 gene
768	2	358	218	1291	g12861800	0	data source:SPTR, source key:P97584, evidence:ISS~homolog to NADP-DEPENDENT LEUKOTRIENE B4 12-HYDROXYDEHYDROGENASE (EC 1.1.1.-) (DITHIOLETHIONE-INDUCIBLE GENE-1)-putative

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
768	2	358	218	1291	g3878713	5.00E-84	weak similarity with quinone oxidoreductase, contains similarity to Pfam domain: PF00107 (Zinc-binding dehydrogenases), Score=-80.6, E-value=6.2e-06, N=1-cDNA EST yk164b4.5 comes from this gene-cDNA EST yk164b4.3 comes from this gene-cDNA EST yk264f3.5 comes from this gene
769	3	420	42	1301	g438007	1.00E-22	alpha-2-macroglobulin receptor
769	3	420	42	1301	g8926243	3.00E-20	low density lipoprotein receptor related protein LRP1B/LRP-DIT
769	3	420	42	1301	g7291057	3.00E-20	CG12139 gene product
770	3	221	3	665	g16553391	1.00E-137	unnamed protein product
770	3	221	3	665	g12483900	4.00E-67	zinc finger protein HIF-4
770	3	221	3	665	g14456631	3.00E-44	dJ54B20.4 (novel KRAB box containing C2H2 type zinc finger protein)
771	1	664	1477	3468	g4589670	0	KIAA1010 protein
771	1	664	1477	3468	g15207833	1.00E-75	hypothetical protein
771	1	664	1477	3468	g12845768	9.00E-63	data source:SPTR, source key:Q9Y2L3, evidence:ISS-homolog to KIAA1010 PROTEIN (FRAGMENT)-putative
772	2	418	1433	2686	g4589678	0	KIAA1014 protein
772	2	418	1433	2686	g10434696	0	unnamed protein product
772	2	418	1433	2686	g6808095	0	hypothetical protein
773	2	276	2	829	g16553765	1.00E-127	unnamed protein product
773	2	276	2	829	g12839186	1.00E-121	data source:SPTR, source key:Q9V560, evidence:ISS-putative-related to CG8576 PROTEIN
773	2	276	2	829	g1072250	5.00E-28	F5381.2 gene product
774	1	636	145	2052	g12804475	0	Similar to spleen tyrosine kinase
774	1	636	145	2052	g12804209	0	Similar to spleen tyrosine kinase
774	1	636	145	2052	g479013	0	protein tyrosine kinase
776	3	225	48	722	g18027350	1.00E-102	unknown
776	3	225	48	722	g15072406	1.00E-102	TNFAIP1-like protein
776	3	225	48	722	g16152040	2.00E-99	polymerase delta-interacting protein 1
777	3	796	276	2663	g1749794	0	serine/threonine protein kinase
777	3	796	276	2663	g14250622	0	Similar to ELKL motif kinase
777	3	796	276	2663	g57920	0	serine/threonine protein kinase
778	2	2067	224	6424	g11596412	0	GAC-1
778	2	2067	224	6424	g4240237	0	KIAA0874 protein

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
778	2	2067	224	6424	g10437204	0	unnamed protein product
779	2	839	284	2800	g16551917	0	unnamed protein product
779	2	839	284	2800	g16356673	0	LIM protein prickle b
779	2	839	284	2800	g14595658	0	LIM protein prickle
780	2	538	2	1615	g11323324	0	dj138B7.3.2 (lethal (3) malignant brain tumor ((3)mbt) protein (Drosophila))
780	2	538	2	1615	g3327176	0	homolog (isoform 2) (KIAA0681))
780	2	538	2	1615	g11323323	0	KIAA0681 protein
781	1	564	118	1809	g5764636	0	dj138B7.3.1 (Continued from dj862K6.1 in Em:AL031681)
781	1	564	118	1809	g12655229	0	DNA binding protein p96PIF
781	1	564	118	1809	g9863866	0	glucocorticoid modulatory element binding protein 1
782	3	428	18	1301	g3327094	1.00E-179	glucocorticoid modulatory element binding protein 1
782	3	428	18	1301	g7381109	1.00E-167	KIAA0640 protein
782	3	428	18	1301	g12653667	1.00E-167	SWAP-70 homolog
783	2	157	2291	2761	g7688677	4.00E-45	SWAP-70 protein
783	2	157	2291	2761	g7578783	4.00E-45	mitochondrial solute carrier
783	2	157	2291	2761	g16506178	2.00E-42	HT015 protein
784	2	238	2	715	g16555334	1.00E-110	mitochondrial solute carrier-like protein
784	2	238	2	715	g16508176	1.00E-110	Rlg protein
784	2	238	2	715	g4235148	1.00E-110	small GTP-binding tumor suppressor 1
785	2	1213	656	4294	g9845485	0	BC41195_1
785	2	1213	656	4294	g14388339	0	protocadherin-9
785	2	1213	656	4294	g13874450	0	hypothetical protein
786	3	212	72	707	g18615326	1.00E-104	hypothetical protein
786	3	212	72	707	g12854500	2.00E-88	unnamed protein product
786	3	212	72	707	g15277499	2.00E-87	Mitochondrial carrier proteins containing protein~data source:Pfam, source key:PF00153, evidence:ISS~putative
787	1	521	241	1803	g16741627	0	Similar to RIKEN cDNA 4930433D19 gene
787	1	521	241	1803	g12859683	0	Similar to RIKEN cDNA 3830421M04 gene
787	1	521	241	1803	g12859683	0	data source:SPTR, source key:Q63615, evidence:ISS~homolog to VACUOLAR PROTEIN SORTING HOMOLOG R-VPS33A~putative
787	1	521	241	1803	g1477468	0	vacuolar protein sorting homolog r-vps33a
788	1	818	1	2454	g11320820	0	VSGP/F-spondin



TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
788	1	818	1	2454	g11320818	0	VSGP/F-spondin
788	1	818	1	2454	g204177	0	f-spondin
789	1	113	211	549	g6714707	1.00E-52	hypothetical protein
789	1	113	211	549	g16589079	1.00E-52	WD repeat protein BIG-3
789	1	113	211	549	g16359284	1.00E-52	Similar to hypothetical protein
790	1	149	145	591	g7959207	2.00E-26	KIAA1473 protein
790	1	149	145	591	g498736	4.00E-26	zinc finger protein
790	1	149	145	591	g16551398	6.00E-26	unnamed protein product
791	1	178	1	534	g16551459	1.00E-100	unnamed protein product
791	1	178	1	534	g7303923	3.00E-25	CG8027 gene product
791	1	178	1	534	g12057020	2.00E-08	putative notch receptor protein
792	3	373	171	1289	g12856757	1.00E-132	data source:SPTR, source key:Q9VKF0, evidence:ISS~putative~related to CG14939 PROTEIN
792	3	373	171	1289	g15788437	1.00E-132	cyclin-box carrying protein
792	3	373	171	1289	g15451434	1.00E-124	hypothetical protein

TABLE 8

Program	Description	Reference	Parameter Threshold
ABI FACTURA	A program that removes vector sequences and masks ambiguous bases in nucleic acid sequences.	Applied Biosystems, Foster City, CA.	
ABI/PARACEL FDF	A Fast Data Finder useful in comparing and annotating amino acid or nucleic acid sequences.	Applied Biosystems, Foster City, CA; Paracel Inc., Pasadena, CA.	Mismatch <50%
ABI AutoAssembler	A program that assembles nucleic acid sequences.	Applied Biosystems, Foster City, CA.	
BLAST	A Basic Local Alignment Search Tool useful in sequence similarity search for amino acid and nucleic acid sequences. BLAST includes five functions: blastp, blastn, blastx, tblastn, and tblastx.	Altschul, S.F. et al. (1990) <i>J. Mol. Biol.</i> 215:403-410; Altschul, S.F. et al. (1997) <i>Nucleic Acids Res.</i> 25:3389-3402.	ESTs: Probability value= 1.0E-8 or less; Full Length sequences: Probability value= 1.0E-10 or less
FASTA	A Pearson and Lipman algorithm that searches for similarity between a query sequence and a group of sequences of the same type. FASTA comprises at least five functions: fasta, tfasta, fastx, tfastx, and ssearch.	Pearson, W.R. and D.J. Lipman (1988) <i>Proc. Natl. Acad. Sci. USA</i> 85:2444-2448; Pearson, W.R. (1990) <i>Methods Enzymol.</i> 183:63-98; and Smith, T.F. and M.S. Waterman (1981) <i>Adv. Appl. Math.</i> 2:482-489.	ESTs: fasta E value=1.06E-6; Assembled ESTs: fasta Identity= 95% or greater and Match length=200 bases or greater; fastx E value=1.0E-8 or less; Full Length sequences: fastx score=100 or greater
BLIMPS	A BLocks IMProved Searcher that matches a sequence against those in BLOCKS, PRINTS, DOMO, PRODOM, and PFAM databases to search for gene families, sequence homology, and structural fingerprint regions.	Henikoff, S. and J.G. Henikoff (1991) <i>Nucleic Acids Res.</i> 19:6565-6572; Henikoff, J.G. and S. Henikoff (1996) <i>Methods Enzymol.</i> 266:88-105; and Attwood, T.K. et al. (1997) <i>J. Chem. Inf. Comput. Sci.</i> 37:417-424.	Probability value= 1.0E-3 or less
HMMER	An algorithm for searching a query sequence against hidden Markov model (HMM)-based databases of protein family consensus sequences, such as PFAM.	Krogh, A. et al. (1994) <i>J. Mol. Biol.</i> 235:1501-1531; Sonnhammer, E.L.L. et al. (1988) <i>Nucleic Acids Res.</i> 26:320-322; Durbin, R. et al. (1998) <i>Our World View, in a Nutshell</i> , Cambridge Univ. Press, pp. 1-350.	PFAM hits: Probability value= 1.0E-3 or less; Signal peptide hits: Score= 0 or greater
ProfileScan	An algorithm that searches for structural and sequence motifs in protein sequences that match sequence patterns defined in Prosite.	Gribskov, M. et al. (1988) <i>CABIOS</i> 4:61-66; Gribskov, M. et al. (1989) <i>Methods Enzymol.</i> 183:146-159; Bairoch, A. et al. (1997) <i>Nucleic Acids Res.</i> 25:217-221.	Normalized quality score≥GCG-specified "HIGH" value for that particular Prosite motif. Generally, score=1.4-2.1.

TABLE 8

Program	Description	Reference	Parameter Threshold
Phred	A base-calling algorithm that examines automated sequencer traces with high sensitivity and probability.	Ewing, B. et al. (1998) <i>Genome Res.</i> 8:175-185; Ewing, B. and P. Green (1998) <i>Genome Res.</i> 8:186-194.	
Phrap	A Phils Revised Assembly Program including SWAT and CrossMatch, programs based on efficient implementation of the Smith-Waterman algorithm, useful in searching sequence homology and assembling DNA sequences.	Smith, T.F. and M.S. Waterman (1981) <i>Adv. Appl. Math.</i> 2:482-489; Smith, T.F. and M.S. Waterman (1981) <i>J. Mol. Biol.</i> 147:195-197; and Green, P., University of Washington, Seattle, WA.	Score= 120 or greater; Match length= 56 or greater
Consed	A graphical tool for viewing and editing Phrap assemblies.	Gordon, D. et al. (1998) <i>Genome Res.</i> 8:195-202.	
SPScan	A weight matrix analysis program that scans protein sequences for the presence of secretory signal peptides.	Nielson, H. et al. (1997) <i>Protein Engineering</i> 10:1-6; Claverie, J.M. and S. Audic (1997) <i>CABIOS</i> 12:431-439.	Score=3.5 or greater
TMAP	A program that uses weight matrices to delineate transmembrane segments on protein sequences and determine orientation.	Persson, B. and P. Argos (1994) <i>J. Mol. Biol.</i> 237:182-192; Persson, B. and P. Argos (1996) <i>Protein Sci.</i> 5:363-371.	
TMHMMER	A program that uses a hidden Markov model (HMM) to delineate transmembrane segments on protein sequences and determine orientation.	Sonnhammer, E.L. et al. (1998) <i>Proc. Sixth Intl. Conf. On Intelligent Systems for Mol. Biol.</i> , Glasgow et al., eds., The Am. Assoc. for Artificial Intelligence (AAAI) Press, Menlo Park, CA, and MIT Press, Cambridge, MA, pp. 175-182.	
Motifs	A program that searches amino acid sequences for patterns that matched those defined in Prosite.	Bairoch, A. et al. (1997) <i>Nucleic Acids Res.</i> 25:217-221; Wisconsin Package Program Manual, version 9, page M51-59, Genetics Computer Group, Madison, WI.	

## CLAIMS

### What is claimed is:

- 5           1. An isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of:
  - a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-396,
  - b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-396,
  - 10       c) a polynucleotide sequence complementary to a),
  - d) a polynucleotide sequence complementary to b), and
  - e) an RNA equivalent of a) through d).
- 15           2. An isolated polynucleotide of claim 1, comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-396.
3. An isolated polynucleotide comprising at least 60 contiguous nucleotides of a polynucleotide of claim 1.
- 20           4. A composition for the detection of expression of disease detection and treatment molecule polynucleotides comprising at least one of the polynucleotides of claim 1 and a detectable label.
5. A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 1, the method comprising:
  - 25       a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and
  - b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.
- 30           6. A method for detecting a target polynucleotide in a sample, said target polynucleotide comprising a sequence of a polynucleotide of claim 1, the method comprising:
  - a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex
  - 35       is formed between said probe and said target polynucleotide or fragments thereof, and

b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.

7. A method of claim 5, wherein the probe comprises at least 30 contiguous nucleotides.

8. A method of claim 5, wherein the probe comprises at least 60 contiguous nucleotides.

9. A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 1.

10. A cell transformed with a recombinant polynucleotide of claim 9.

11. A transgenic organism comprising a recombinant polynucleotide of claim 9.

12. A method for producing a disease detection and treatment molecule polypeptide, the method comprising:

a) culturing a cell under conditions suitable for expression of the disease detection and treatment molecule polypeptide, wherein said cell is transformed with a recombinant polynucleotide of claim 9, and

b) recovering the disease detection and treatment molecule polypeptide so expressed.

13. A purified disease detection and treatment molecule polypeptide (MDDT) encoded by at least one of the polynucleotides of claim 2.

14. An isolated antibody which specifically binds to a disease detection and treatment molecule polypeptide of claim 13.

15. A method of identifying a test compound which specifically binds to the disease detection and treatment molecule polypeptide of claim 13, the method comprising the steps of:

a) providing a test compound;

b) combining the disease detection and treatment molecule polypeptide with the test compound for a sufficient time and under suitable conditions for binding; and

c) detecting binding of the disease detection and treatment molecule polypeptide to the test compound, thereby identifying the test compound which specifically binds the disease detection and treatment molecule polypeptide.

16. A microarray wherein at least one element of the microarray is a polynucleotide of claim

3.

17. A method for generating a transcript image of a sample which contains polynucleotides,  
5 the method comprising the steps of:

- a) labeling the polynucleotides of the sample,
- b) contacting the elements of the microarray of claim 16 with the labeled polynucleotides of the sample under conditions suitable for the formation of a hybridization complex, and
- c) quantifying the expression of the polynucleotides in the sample.

10

18. A method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a polynucleotide sequence of claim 1, the method comprising:

- a) exposing a sample comprising the target polynucleotide to a compound, under conditions  
15 suitable for the expression of the target polynucleotide,
- b) detecting altered expression of the target polynucleotide, and
- c) comparing the expression of the target polynucleotide in the presence of varying amounts of the compound and in the absence of the compound.

19. A method for assessing toxicity of a test compound, said method comprising:

- a) treating a biological sample containing nucleic acids with the test compound;
- b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide of claim 1 under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological  
25 sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide of claim 1 or fragment thereof;
- c) quantifying the amount of hybridization complex; and
- d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount  
30 of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

20. An array comprising different nucleotide molecules affixed in distinct physical locations on a solid substrate, wherein at least one of said nucleotide molecules comprises a first oligonucleotide or polynucleotide sequence specifically hybridizable with at least 30 contiguous nucleotides of a target  
35 polynucleotide, said target polynucleotide having a sequence of claim 1.

21. An array of claim 20, wherein said first oligonucleotide or polynucleotide sequence is completely complementary to at least 30 contiguous nucleotides of said target polynucleotide.

22. An array of claim 20, wherein said first oligonucleotide or polynucleotide sequence is  
5 completely complementary to at least 60 contiguous nucleotides of said target polynucleotide

23. An array of claim 20, which is a microarray.

24. An array of claim 20, further comprising said target polynucleotide hybridized to said first  
10 oligonucleotide or polynucleotide.

25. An array of claim 20, wherein a linker joins at least one of said nucleotide molecules to said solid substrate.

15 26. An array of claim 20, wherein each distinct physical location on the substrate contains multiple nucleotide molecules having the same sequence, and each distinct physical location on the substrate contains nucleotide molecules having a sequence which differs from the sequence of nucleotide molecules at another physical location on the substrate.

20 27. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

- a) an amino acid sequence selected from the group consisting of SEQ ID NO:397-792,
- b) a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:397-792,
- 25 c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:397-792, and
- d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:397-792.

30 28. An isolated polypeptide of claim 27, comprising a polypeptide sequence selected from the group consisting of SEQ ID NO:397-792.

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